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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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867 86.1 168 18 AAW36048 Mouse bcl-w F	BCT-7		22	239	0	10.	42
867 86.1 168 18 AAW35048 Amino acid seed 433 5 43.0 411 22 AAW059219 AAW5984 Amino acid seed 433 5 42.6 233 16 AAW68887 Acid 223 17 AAW05821 Acid 224 AAW05821 Acid 233 18 AAW31530 Acid 225 AAW65821 Acid 233 21 AAW32323 Acid 226 Acid 233 21 AAW32323 Acid 226 Acid 233 22 AAB473303 Acid 226 Acid 233 22 AAB473304 Acid 236 Acid 237 Acid 237 Acid 237 Acid 238 Acid 239 22 AAB473303 Acid 239 22 AAB473303 Acid 239 22 AAB473303 Acid 239 22 AAB473313 Acid 239 23 AAB473313 Acid 239 23 AAB473313 Acid 239 23 AAB473313 Acid 239 Acid 239 24 AAB473313 Acid 239 24 AAB47333 Acid 239 24 AAB473313 Acid 239 24 AAB473313 Acid 239 24 AAB47331 Acid 23	BCL-2		22	239	0	10.	41
867 86.1 168 18 AAW35048 Mouse bcl-w pr 768 76.1 365 19 AAW39884 Amino acid seq 433 5 42.6 233 16 AAR68887 Human thymus B 428.5 42.6 233 17 AAW35223 428.5 42.6 233 18 AAW31530 Human anti-app 428.5 42.6 233 21 AAW39223 428.5 42.6 233 21 AAW39223 428.5 42.6 233 22 AAR64262 428.5 42.6 233 22 AAR64262 428.5 42.6 233 22 AAR673303 Human Bcl-xL pr 428.5 42.6 233 22 AAR673303 Human Bcl-z p 428.5 42.6 233 22 AAR673304 Human Bcl-z p 428.5 42.6 233 22 AAR673304 Mutant rat Bcl 428.5 42.6 233 22 AAR673304 Mutant rat Bcl 428.5 42.6 233 22 AAR673304 Human Bcl-z 428.5 42.6 233 22 AAR673307 Human Bcl-2 p 410.5 40.8 239 20 AAR97812 410.5 40.8 239 16 AAR71301 Human Bcl-2 p 410.5 40.8 239 16 AAR71301 Human Bcl-2 p 410.5 40.8 239 19 AAW897812 410.5 40.8 239 22 AAG64035 Human Bcl-2 p	bcl		22	239			40
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867 86.1 168 18 AAW35048 Amino acid seq 433 5 43.0 411 22 AAU00219 Bcl-xl-TrR apolypept 428.5 42.6 233 16 AAW35887 Human thymus B 428.5 42.6 233 17 AAW3523 Human Bcl-xL protein 428.5 42.6 233 18 AAW31530 Human anti-apolypept 428.5 42.6 233 21 AAY83223 Human Bcl-xL protein 428.5 42.6 233 21 AAY8323 Human Bcl-xL protein 428.5 42.6 233 22 AAB73303 Human Bcl-xL protein encode 428.5 42.6 233 22 AAB73303 Human Bcl-xL protein encode 428.5 42.6 233 22 AAB73304 Human Bcl-zL protein encode 428.5 42.6 233 22 AAB73304 Human Bcl-2 protein encode 5 dcl protein 428.5 42.2 235 18 AAW13396 Protein encode 648.5 42.2 235 22 AAB35131 Muran Bcl-2 protein encode 648.5 41.0 239 22 AAB35131 Muran Bcl-2 protein encode 648.5 41.0 239 22 AAB35130 Human Bcl-2 protein encode 648.5 41.0 239 22 AAB35130 Human Bcl-2 protein encode 648.5 41.0 239 22 AAB35130 Human Bcl-2 protein encode 648.5 41.0 239 22 AAB35130 Human Bcl-2 protein encode 648.5 41.0 239 24 AAB7312 Human Bcl-2 protein encode 648.5 41.0 239 24 AAB7312 Human Bcl-2 protein encode 648.5 41.0 239 24 AAB7312 Human Bcl-2 protein encode 648.5 41.0 239 16 AAB711404 Human Bcl-2 protein encode 648.5 41.0 239 16 AAB711404 Human Bcl-2 protein encode 648.5 41.0 239 16 AAB711404 Human Bcl-2 protein encode 648.5 41.0 239 16 AAB711404 Human Bcl-2 protein encode 648.5 41.0 239 16 AAB711404 Human Bcl-2 protein encode 648.5 41.0 239 22 AAB55130 Human Bcl-2 protein encode 648.5 41.0 239 22 AAB55130 Human Bcl-2 protein encode 648.5 41.0 239 22 AAB55130 Human Bcl-2 protein encode 648.5 41.0 239 22 AAB55130 Human Bcl-2 protein encode 648.5 41.0 239 22 AAB55130 Human Bcl-2 protein encode 648.5 41.0 239 22 AAB55130 Human Bcl-2 protein encode 648.5 41.0 239 22 AAB55130 Human Bcl-2 protein encode 648.5 41.0 239 22 AAB55130 Human Bcl-2 protein encode 648.5 41.0 239 22 AAB55130 Human Bcl-2 protein encode 648.5 41.0 239	BCL		22	239		10.	ა 8
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867 86.1 168 18 AAW35048 Mouse bcl-w pr 766 76.1 365 19 AAW3984 Amino acid seq 433.5 42.6 233 16 AAR68887 Human thymus B 428.5 42.6 233 17 AAW05821 428.5 42.6 233 17 AAW31530 428.5 42.6 233 21 AAW31530 428.5 42.6 233 21 AAY83923 428.5 42.6 233 21 AAY839269 428.5 42.6 233 22 AAG4262 428.5 42.6 233 22 AAG4262 428.5 42.6 233 22 AAG54262 428.5 42.6 233 22 AAG54353 428.5 42.6 233 22 AAB73303 428.5 42.6 233 22 AAB73130 428.5 42.6 233 22 AAB73304 Human Bcl-xL [Ref. Str. Str. Str. Str. Str. Str. Str. Str	human BCI-		20	239		0	36
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867 86.1 168 18 AAW35048 Mouse bcl-w p 766 76.1 36 19 AAW59884 Amino acid set 433.5 42.6 233 16 AAR68887 Human thymus 428.5 42.6 233 17 AAW05921 Human anti-ap 428.5 42.6 233 18 AAW31330 Bcl-x polypep 428.5 42.6 233 21 AAY69269 Human Bcl-xL 428.5 42.6 233 21 AAY69369 Human Bcl-xL 428.5 42.6 233 22 AAB73303 Human Bcl-xL 428.5 42.6 233 22 AAB73303 Human Bcl-xL 428.5 42.6 233 22 AAB73303 Human Bcl-xL 428.5 42.6 233 22 AAB73304 Human Bcl-xL 428.5 42.6 233 22 AAB73304 Human Bcl-xL 428.5 42.6 233 22 AAB7310 Human Bcl-xL	BCI-2.		22	236	•	413	27
867 86.1 168 18 AAW35048 Mouse bcl-w p 76 76.1 365 19 AAW5984 Amino acid se 43.5 43.0 4411 22 AAU00219 428.5 42.6 233 16 AAR68887 Human thymus 428.5 42.6 233 17 AAW05921 428.5 42.6 233 18 AAW31530 Human anti-ap 428.5 42.6 233 18 AAW31530 Human anti-ap 428.5 42.6 233 21 AAY83923 Human Bcl-XL 428.5 42.6 233 22 AAB73303 428.5 42.6 233 22 AAB73303 Rat wild-type 428.5 42.6 233 22 AAB73303 Human Bcl-XL 428.5 42.6 233 22 AAB73303 Rat wild-type 428.5 42.6 233 22 AAB73303 Human Bcl-XL 428.5 42.6 233 22 AAB73304 Human Bcl-XL 428.5 42.6 233 22 AAB73303 Rat wild-type 428.5 42.6 233 22 AAB73304 Human Bcl-XL 428.5 42.6 233 22 AAB73304 Human Bcl-XL 428.5 42.6 233 22 AAB7315 Protein encode 428.5 42.2 235 18 AAW19396 "Deprenyl" (F 428.5 42.2 233 22 AAB7314 Mutant rat Bc	cr-2 pro		22	239		416.5	26
867 86.1 168 18 AAW35048 Mouse bcl-w p 766 76.1 365 19 AAW59884 Amino acid see 433 5 43.0 441 22 AAU00219 428.5 42.6 233 16 AAR68887 Human thymus 428.5 42.6 233 17 AAW05921 Bcl-xL protei 428.5 42.6 233 18 AAW31530 Bcl-xL polypep 428.5 42.6 233 21 AAY83223 428.5 42.6 233 22 AAB62052 428.5 42.6 233 22 AAB73303 Human Bcl-xL 428.5 42.6 233 22 AAB73103 Human Bcl-xL 428.5 42.6 233 22 AAB47310 Human Bcl-xL	٠.		22	233		424.5	25
867       86.1       168       18       AAW35048       Mouse bcl-w p         766       76.1       36       19       AAW59884       Amino acid see         433.5       43.0       411       22       AAU00219       Human thymus         428.5       42.6       233       16       AAR68887       Human thymus         428.5       42.6       233       17       AAW65821       Human anti-ap         428.5       42.6       233       18       AAW311330       Human anti-ap         428.5       42.6       233       21       AAY89223       Human anti-ap         428.5       42.6       233       21       AAY869969       Human Bcl-xL         428.5       42.6       233       22       AAB64862       Human anti-xL         428.5       42.6       233       22       AAB64862       Human anti-ap         428.5       42.6       233       23       AAB64862       Human anti-ap         428.5       42.6       233       22       AAB64862       AR86888         428.5       42.6       233       22       AAB64862       AR86888         428.5       42.6       233       22       AAB6			18	225		425	24
867       86.1       168       18       AAW35048       Mouse bcl-w p         76       76.1       365       19       AMS9884       Amino acid se         43.5       43.0       4411       22       AAU00219       Bcl-Xl-DTR ap         428.5       42.6       233       16       AAR68887       Human thymus         428.5       42.6       233       17       AAW05821       Bcl-XL protei         428.5       42.6       233       18       AAW31530       Human anti-ap         428.5       42.6       233       21       AAY83223       Bcl-x polypep         428.5       42.6       233       21       AAY69969       Human Bcl-XL         428.5       42.6       233       22       AAB73303       Rat wild-type         428.5       42.6       233       22       AAB50338       Human Bcl-XL         428.5       42.6       233       22       AAB50338       Human Bcl-XL	Protein encoded		22	233		428.5	23
867 86.1 168 18 AAW35048 Mouse bcl-w p 766 76.1 365 19 AAW59884 Amino acid see 433 5 43.0 4411 22 AAU00219 Bcl-XL-DTR ap 428.5 42.6 233 16 AAR68887 Human thymus 428.5 42.6 233 17 AAW05921 Bcl-XL protei 428.5 42.6 233 18 AAW31530 Human anti-ap 428.5 42.6 233 21 AAY83223 428.5 42.6 233 21 AAY83223 428.5 42.6 233 21 AAY6969 428.5 42.6 233 22 AAB64262 428.5 42.6 233 22 AAB674262 Human Bcl-XL 428.5 42.6 233 22 AAB674262	Human BCI~XL pr		22	233		428.5	22
867 86.1 168 18 AAW35048 Mouse bcl-w p 766 76.1 368 19 AAW59884 Amino acid see 433.5 43.0 411 22 AAU00219 Bcl-xl-DTR ap 428.5 42.6 233 16 AAR68887 Human thymus 428.5 42.6 233 17 AAW05821 Bcl-xL protest 428.5 42.6 233 18 AAW31330 Bcl-x polypep 428.5 42.6 233 18 AAW395963 Human mcl-xL 428.5 42.6 233 21 AAY69969 Human Bcl-xL 428.5 42.6 233 21 AAY6912 Human Bcl-xL 428.5 42.6 233 21 AAY6912 Human Bcl-XL 428.5 42.6 233 21 AAY6912 Human Bcl-XL	wild-type	AAB7330	22	233		428.5	21
867       86.1       168       18       AAW35048       Mouse bcl.w p.         76       76.1       365       19       AAW55984       Amino acid se         43.5       43.0       411       22       AAU00219       Bcl.XL-DTR ap         428.5       42.6       233       16       AAR68887       Human thymus         428.5       42.6       233       17       AAW05821       Human anti-ap         428.5       42.6       233       18       AAW31330       Human anti-ap         428.5       42.6       233       21       AAY69969       Bcl.x polypep         428.5       42.6       233       21       AAY69969       Human Bcl.L.	an BCI-XL	AAG6426	22	233		428.5	20
867 86.1 168 18 AAW35048 Mouse bcl-w p. 766 76.1 365 19 AAW59884 Amino acid see 43.3 5 43.0 411 22 AAU00219 Bcl-XL-DTR ap. 428.5 42.6 233 16 AAR68887 Human thymus 428.5 42.6 233 17 AAW05821 Human anti-parts 428.5 42.6 233 18 AAW31530 Human anti-parts 428.5 42.6 233 18 AAW31530 Human anti-parts 428.5 42.6 233 21 AAY83223 Bcl-x polypep.	BCT-XT		21	233		428.5	19
867 86.1 168 18 AAW36048 Mouse bcl-v 766 76.1 365 19 AAW59884 Amino acid 433.5 43.0 411 22 AAU0219 Bcl-X1-DTR 428.5 42.6 233 16 AAR68887 Human thym 428.5 42.6 233 17 AAW05891 Bcl-XL pro 428.5 42.6 233 18 AAW31530 Human anti	ротурер		21	233		428.5	18
867 86.1 168 18 AAW36048 Mouse bcl-v 768 76.1 365 19 AAW59884 Amino acid 43.0 411 22 AAU00219 Bcl-Xl-DTR 428.5 42.6 233 16 AAR68887 Human thym 428.5 42.6 233 17 AAW05821 Bcl-XL pro			18	233		428.5	17
867 86.1 168 18 AAW36048 Mouse bcl-v 766 76.1 365 19 AAW59884 Amino acid 43.5 43.0 411 22 AAU00219 Bcl-x1-DTR 428.5 42.6 233 16 AAR68887 Human thym	Bc1-XL protein.		17	233	٠	428.5	16
867 86.1 168 18 AAW36048 Mouse bcl-v 766 76.1 365 19 AAW59884 Amino acid 433.5 43.0 411 22 AAU00219 Bcl-xl-DTR	Human Enymus BC		16	233	•	428.5	15
867 86.1 168 18 AAW36048 Mouse bcl-v 766 76.1 365 19 AAW59884 Amino acid	XL-DTR		22	411	ω.	433.5	14
867 86.1 168 18 AAW36048 Mouse bcl-w	o acid		19	365	<u>o</u>	766	<u>1</u> 3
	bcl-w		18	168	6	867	12

## ALIGNMENTS

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RESULT
AAY05530
PG XXX
                                                                                                                                                                                                                                                                                                         AAY05530 standard; Protein; 193 AA.
                                                                                                                                                                                                                          Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
                                                                                                                                                                                                                                              Human Bcl-w protein essential for spermatogenesis.
                                                                                                                                                                                                                                                                 05-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                     AAY05530;
                 An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w \,
                                                                                                                                                                                                                   animal model.
                                               WPI; 1999-243890/20.
N-PSDB; AAX25132.
                                                                            Adams J,
                                                                                              (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                   16-SEP-1997;
                                                                                                                                      16-SEP-1998;
                                                                                                                                                        25-MAR-1999
                                                                                                                                                                            WO9913710-A1
                                                                                                                                                                                               Homo sapiens
                                                                            Cory S, Gibson L,
                                                                                                                   97AU-0009228.
                                                                                                                                       98WO-AU00764.
                                                                            Koentgen F, Print C;
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Claim 2; Page 33; 52pp; English

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ACC XXX ACC XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
Nucleic acids encoding B-cell lymphoma-y protein -
                                                                                                                                                           Guastella J;
                                                                                                                                                                                                                                                                           23-FEB-1996;
11-FEB-1997;
                                                                    N-PSDB;
                                                                                                WPI; 1998-446079/38
                                                                                                                                                                                                                                                                                                                                                                  11-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                             04-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US5789201-A
                                                                                                                                                                                                                (COCE-) COCENSYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bcl-y; bcl-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human bcl-y protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW61392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW61392 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is human Bcl-w, Bcl-2 family which is widely.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 GALVTVGAFFASK 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l matpasapdtralvadfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEDLVG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell death pathway; apoptotic; apoptosis; human.
                                                                                                                                                                                                                                                                        96US-0012201.
97US-0798897.
                                                                                                                                                                                                                                                                                                                                                               97US-0798897.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                        23-FEB-1996;
11-FEB-1997;
25-NOV-1997;
              Guastella J;
                                                                                                                                                                                                                                                                   Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                           (COCE-) COCENSYS INC
                                                                                                                                      25-NOV-1997;
                                                                                                                                                                    16-MAR-1999.
                                                                                                                                                                                                 US5883229-A.
                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                           parasite.
                                                                                                                                                                                                                                                                                                                                                                                              The human bcl-y protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW97392 standard; Protein; 193
                                                                                                                                                                                                                                                                                                                                                                                                                                  20-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'The mammalian bcl-y protein is a member of the bcl-2 family, components in the cell death pathway. The bcl-2 family have both apoptotic activit and the apoptosis blocking activity. bcl-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also antisense constructs can be used in disorders where prevention of cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      producing recombinant protein for use in treating uncontrolled cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           death is desired.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The mammalian bcl-y protein is a member of the bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example; Column 17/18; 27pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 matpasapdtralvedfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                       96US-0012201.
97US-0798897.
97US-0978523.
                                                                                                                                    97US-0978523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1002; DB 19;
Pred. No. 9.3e-103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 193;
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RESULT
ANW350/T
ID AAW37
XX AAW3
AC AAW3
AC AAW3
XX BCl.
XX BCl.
XX Gias
DE Huma
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PN WO9
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XX 27-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents human bcl-y protein (Hbcl-y). The CC specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in CC proteins may be used to treat conditions associated with a disruption of CC the cell death pathway. If they act as cell death inhibitors, they may be used in therapies to treat subjects suffering from: strokes, head trauma, CC ell death, pathway. If they act as cell death inhibitors, they may be CC (especially multiple sclerosis), myocardial infarction, vitally induced CC cell death, aging, spinal cord injuries and amyotrophic lateral CC sclerosis conditions where cells under go premature cell death as a CC result of triggers which may or may not be apparent. They may also be CC used in this way to develop cell lines which remain viable in culture for CC an extended period. In contrast, if they act as cell death stimulators, Rbcl-y and Hbcl-y may be used to treat conditions associated with CC prolonged cell life span such as cancer (especially kaposi's sarcoma and CC ling cancer) and auto/hyperimmune diseases. They may also be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                   Q
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-214150/18.
N-PSDB; AAX15946.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Columns 17-18; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel bcl-y homologues of the rat and human bcl-2 protein \, - useful for modulating programmed cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cause cell death in, and hence control, parasites.
                                                                                                                                                                             Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
                                                                                                                                                                                                                                                      22-APR-1998
                                                                                                                                                                                                                                                                                     AAW36047;
                                                                                                                                                                                                                                                                                                                    AAW36047 standard; Protein; 193 AA
   27-MAR-1996;
                                                                                                   W09735971-A1
                                                                                                                                   Homo sapiens
                                                                                                                                                                 diagnosis; degenerative
                                                                                                                                                                                                                  Human bcl-w protein.
                                   27-MAR-1997;
                                                                     02-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                     181 galvtvgaffask 193
                                                                                                                                                                                                                                                                                                                                                                                                                                     181 GALVTVGAFFASK 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                    (first entry)
                                   97WO-AU00199
   96AU-0008965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.5%;
                                                                                                                                                                      disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1002; DB 20; Pred. No. 9.3e-103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 193;
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QY
                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                      AAY05531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bcl-2 gene family and extracted from an adult brain library. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis, antibody production or screening of potential modulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1997-489635/45.
N-PSDB; AAT96577.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a novel human protein, bcl-w, encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 48; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           degenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMRA-) AMRAD OPERATIONS PTY LTD.
                                                                                                                                                             Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
                                                                                                                                                                                                                   05-JUL-1999
                                                                                                                                                                                                                                                                         AAY05531 standard; Protein; 193 AA
                                                                                                                                                animal model.
                                                                                                                                                                                        Mouse Bcl-w protein essential for spermatogenesis
                                                                                                                     Mus sp.
             16-SEP-1997;
                                       16-SEP-1998;
                                                                 25-MAR-1999
                                                                                           WO9913710-A1
                                                                                                                                                                                                                                                                                                                                                                       181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         {\tt 1} \verb| matpasapdtralvadfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                                                                                                                    G
                                                                                                                                                                                                                                                                                                                                                          GALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                            QVQEWNVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                                                                                                                                                                                                                                                                                                                                                191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cory S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                    (first entry)
              97AU-0009228
                                       98WO-AU00764.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gibson LM, Holmgreen SP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.3%;
99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1000; DB 18;
Pred. No. 1.6e-102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 193;
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Best Local
                                                                                                                 Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;
                                                   WO9913710-A1
                                                                                                                                             Human Bcl-w protein essential for spermatogenesis.
16-SEP-1998;
                           25-MAR-1999
                                                                               Homo sapiens
                                                                                                           animal model
                                                                                                                                                                               05-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bel-w gene (see AAX25132-35) or in a gene associated with bel-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce
                                                                                                                                                                                                         AAY05532;
                                                                                                                                                                                                                               AAY05532 standard; Protein; 193 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is mouse Bcl-w, a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                        181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein associated with Bcl-w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An animal model exhibiting reduced levels of a Bcl-w protein and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                                                                                                                                                                                                                                                       1 matpastpdtralvadfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MATPASAPDTRALVADFVGYKLROKGYVCGAGPGEGPAADPLHOAMRAAGDEFETRERRT 60
                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                               GALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                   galvtvgaffask 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                           (first entry)
98WO-AU00764.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1000; DB 20;
Pred. No. 1.6e-102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Print C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193;
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                                                                                                                                                                                                                                                  RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is described of a derivative of human Bcl-w
C (see also AAV05530), a pro-survival member of the Bcl-2 family that
C is widely expressed and which is essential for spermatogenesis.
C fie invention relates generally to a method of treatment and to an
C animal model for the identification of molecules and genetic
Sequences useful for inducing or reducing fertility of male animals.
C methods are provided for the treatment of infertility, or for
reducing fertility, by modulating spermatogenesis. An animal model
C carries a mutation is at least one allele of the human or murine
C bcl-w gene (see AAX25132-35) or in a gene associated with bcl-w.
C Such animals have disorganised seminferous tubules and are
Substantially infertile, but possess no other major abnormalities
as determined by histological examination. They can be used to
capable of inducing, enhancing or otherwise facilitating
c spermatogenesis in animals, or which can induce infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                    Mammalian bcl-y protein.
                                                                                                                                                      20-MAY-1999
                                                                                                                                                                                     AAW97394;
                                                                                                                                                                                                              AAW97394 standard; Protein; 192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                          181 GALVTVGAFFASK 193
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                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 37; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein associated with Bcl-w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An animal model exhibiting reduced levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAX25134
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                                                                                                                                                                                                                                                                                                                                                                                                                       61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1\, matpasapdtralvadfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                  7
                                                                                                                                                                                                                                                                                                                                                                   QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                                                                                                                                                                                                                                              galvtvgaffask 193
                                                                                                                                                                                                                                                                                                                                                                                                                                              FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                                                                                                                            qvqewmvayletrlvdwihssggwaeftalygdgaleearrlregnwasvrtvltgaval
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1999-243890/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                   (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97AU-0009228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gibson L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.3%;
99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1000; DB 20;
Pred. No. 1.6e-102;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koentgen F, Print C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of a Bcl-w protein and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y, bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span;

Kaposi's sarcoma; lung

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The present sequence represents a mammalian bcy-1 protein.

CC The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y composed (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein composed to be involved in programmed cell death (apoptosis and necrosis). CC thought to be involved in programmed cell death (apoptosis and necrosis). CC with a disruption of the cell death pathway. If they act as cell death composed cell death as treat conditions associated cell death as treat conditions associated cell death as treat subjects suffering cells. They may be used in therapies to treat subjects suffering cells: they may be used in therapies to treat subjects suffering cells: they may vitally induced cell death, aging, spinal cord injuries and cell death as a result of triggers which may or may not be apparent. CC cell death as a result of triggers which may or may not be apparent. CC viable in culture for an extended period. In contrast, if they act as cell death stimulators, Rbcl-y and Hbcl-y may be used to treat conditions associated with prolonged cell life span such as cancer (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune ccl diseases. They may also be used to cause cell death in, and hence
             RESULT
AAW61391
                                                                                                                                     В
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                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                      Query Match
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11-FEB-1997;
25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guastella J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Columns 19-22; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for modulating programmed cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel bcl-y homologues of the rat and human bcl-2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-214150/18
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                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                              control, parasites.
AAW61391 standard; Protein; 193 AA.
                                                                                                                                  181 alvtvgaffask 192
                                                                                                         182 ALVTVGAFFASK 193
                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                        8
                                                                                                                                                                                              SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121
                                                                                                                                                                                                                                                                                                                                                                                                       192 AA;
                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-0012201.
97US-0798897.
97US-0978523.
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                                                                                                                                                                                                                                                                                                                                         99.0%; Score 997; DB 20; Length 192; 99.5%; Pred. No. 3.3e-102;
                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                  AAW97391
                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                              Matches 190; Conservative
                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW61391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat bcl-y protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-FEB-1996;
11-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-AUG-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US5789201-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. antisense constructs can be used in disorders where prevention of constructs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Guastella J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The mammalian bcl-y protein is a member of the bcl-2 family, components in the cell death pathway. The bcl-2 family have both apoptotic activity and the apoptosis blocking activity. bcl-y falls in the apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example; Fig 3A; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               growth e.g. cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding B-cell lymphoma-y protein - useful for producing recombinant protein for use in treating uncontrolled cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-446079/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (COCE-) COCENSYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                             death is desired.
                          AAW97391;
                                                     AAW97391 standard; Protein; 193 AA.
20-MAY-1999
                                                                                                                       181 galvtvgaffask 193
                                                                                                                                                                           121 QVQEWMYAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                                                                                                  181 GALVTVGAFFASK 193
                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                           61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                      1 matpastpdtralvadfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60
                                                                                                                                                                                                                                                                                                     1 MATDASAPDTRALVADFYGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                 9
                                                                                                                                                                                                                                 fs dlaaq lhvtp gs aqqrftqvs delfqggpn wgrlvaffvfgaal caes vnkeme plvg\\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        V283333
                                                                                                                                                                                                                                                                                                                                                                                                                     193 AA;
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97US-0798897.
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                                                                                                                                                                                                                                                                                                                                                                98.9<del>8</del>;
98.4<del>8</del>;
                                                                                                                                                                                                                                                                                                                                                Score 996; DB 19; Length 193;
pred. No. 4.3e-102;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell
                                                                                                                                                                                                                                              120
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The rat bcl-y protein.

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The present sequence represents rat bcl-y protein (Rbcl-y). The Specification also describes human bcl-y protein (Rbcl-y). Rbcl-y and the specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and the specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and the specification describes and necrosis). Rbcl-y and Hbcl-y composed to treat conditions associated with a disruption of the cell death pathway. If they act as cell death inhibitors, they may be composed in the rapies to treat subjects suffering from: strokes, head trauma, composed to treat subjects suffering from: strokes, head trauma, composed the strokes of the subjects suffering from: strokes, head trauma, composed the strokes of the subjects suffering from: strokes, head trauma, composed the strokes of the subjects suffering from: strokes, head trauma, composed the strokes of the subjects suffering from: strokes, head trauma, composed to the subjects suffering from: strokes, head trauma, composed cell interest conditions associated death as a composed cell interest of the subjects and auto/hyperimmune diseases. They may also be used to treat conditions associated with the subjects and auto/hyperimmune diseases. They may also be used to the subjects and auto/hyperimmune diseases. They may also be used to the subjects and subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-FEB-1996;
11-FEB-1997;
25-NOV-1997;
                                                   121 QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Columns 15-18; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel bcl-y homologues of the rat and human bcl-2 protein for modulating programmed cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAX15945
                                                                                                                            61
                                                                                                                                  61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-214150/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (COCE-) COCENSYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; againg; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                                                                                                                                                                                      1 matpastpdtralvadfvgyklrgkgyvcgagpgegpaadplhqamraagdefetrfrrt 60
                                                                                                                                                                                                                                   1 MATPASAPDTRALVADEVGYKLROKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRERRT 60
fsdlaaqlhvtpgsaqqrftqvsdelfqggpnwgrlvaffvfgaalcaesvnkemeplvg 120
                                                                                                                                                                                                                                                                                                                                190;
                                                                                                                                                                                                                                                                                                                                                   h 98.9%;
Similarity 98.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 AA;
                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-0012201.
97US-0798897.
97US-0978523.
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    Mismatches

                                                                                                                                                                                                                                                                                                                                        Score 996; DB 20;
Pred. No. 4.3e-102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   parasites
                                                                                                                                                                                                                                                                                                                                                                   DB 20; Length 193;
                                                                                                                                                                                                                                                                                                                     Indels

    useful

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                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                             0;
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20 В Qy В Qy

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Query Match Best Local (

Local Similarity

98.4%; 98.4%;

Conservative

1; Mismatches

0, Gaps

0;

Score 991; DB 20; Length 192; Pred. No. 1.5e-101;

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The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein CC thought to be involved in programmed cell death (apoptosis and necrosis). CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated CC inhibitors, they may be used in therapies to treat subjects suffering CC degenerative diseases (especially multiple sclerosis), myocardial CC degenerative diseases (especially multiple sclerosis), myocardial CC amyotrophic lateral sclerosis. Conditions where cells under go premature CC rely may also be used in this way to develop cell lines which remain CC conditions associated with prolonged cell life span such as cancer CC (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune CC constrol passes sarcoma and lung cancer) and auto/hyperimmune CC constrol passes sarcoma and lung cancer) and auto/hyperimmune CC constrol passes sarcoma and lung cancer) and auto/hyperimmune CC constrol passes sarcoma and lung cancer) and auto/hyperimmune CC constrol passes sarcoma and lung cancer) and auto/hyperimmune CC constrol passes sarcoma and lung cancer) and auto/hyperimmune CC constrol passes sarcoma and lung cancer) and auto/hyperimmune CC constrol passes sarcoma and lung cancer) and auto/hyperimmune CC constrol passes sarcoma and lung cancer) and auto/hyperimmune CC constrol passes sarcoma and lung cancer) and auto/hyperimmune cCC constrol passes sarcoma and lung cancer) and auto/hyperimmune cCC constrol passes sarcoma and lung cancer) and auto/hyperimmune cCC constrol passes sarcoma and lung cancer) and auto/hyperimmune cCC constrol passes sarcoma and lung cancer) and auto/hyperimmune cCC constrol passes sarcoma and lung cancer) and auto/hyperimmune cCC constrol passes sarcoma and cause cell death in, and hence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW97393
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Columns 19-20; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel bcl-y homologues of the rat and human bcl-2 protein - useful for modulating programmed cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-214150/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (COCE-) COCENSYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-FEB-1996;
11-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US5883229-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein sequence of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW97393 standard; Protein; 192 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW97393;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 GALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10
192 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-0012201.
97US-0798897.
97US-0978523.
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RESULT 11
AAY05533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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                                    The present sequence is described of a derivative of mouse Bcl-w (see also AAY05531), a pro-survival member of the Bcl-2 family that CC (see also AAY05531), a pro-survival member of the Bcl-2 family that CC is widely expressed and which is essential for spermatogenesis.

CC The derivative lacks the 24 vterminal amino acids of Bcl-w.

CC The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic consequences useful for inducing or reducing fertility of male animals.

CC Sequences useful for the treatment of infertility, or for machine an expression of the treatment of infertility, or for machine and the consequence of the human or murine consequence and the provided for the treatment of the human or murine constant and the consequence of the human or murine constant and the consequence of the human or murine constant and the consequence of the human or murine consequence is substantially infertile, but possess no other major abnormalities consequence of the consequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09913710-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse Bcl-w protein deritvative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY05533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY05533 standard; Protein; 192 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                An animal model exhibiting reduced levels of a Bcl-w protein and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein associated with Bcl-w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAX25135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 alvtvgaffask 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 39; 52pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1999-243890/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW36048 standard; Protein; 168 AA
                                                                                   This sequence represents a novel protein, bcl-w, encoded by the mouse bcl-2 gene family. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis, antibody production or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosis; degenerative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW36048;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adams JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding apoptosis related gene bcl-w - used to induce or inhibit cell survival, e.g. for treatment of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AMRA-) AMRAD OPERATIONS PTY LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 50-51; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    degenerative diseases
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                                                               screening of potential modulators.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cory S, Gibson LM, Holmgreen SP;
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Query Match

86.1%;

Score 867;

DB 18;

Length 168;

Sequence

168 AA;

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                                                  Matches
                                                                          Query Match
                                                                                                                  Sequence
                                                                                                                                             This is the amino acid sequence of the cDNA clone Bcl-like (HAICH29), used in the method of the invention. The products of the clone can be used for treating conditions associated with abnormal expression of the polypeptides. They can be used for e.g. treating chronic inflammatory diseases, immunological disorders, autoimmune diseases, inflammatory diseases, various allergies, and as anti-infectious agents.
                                                                                                                                                                                                                                              Claim 1; Fig 12A-12D; 120pp; English.
                                                                                                                                                                                                                                                                                  New isolated polynucleotides and encoded polypeptides - used to develop products for treating e.g. inflammatory diseases, infections, immunological disorders, autoimmune diseases, allergies
                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAV41925.
                                                                                                                                                                                                                                                                                                                                                                                                                            ( HUMA - )
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21-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                         (AUCK-) AUCKLAND UNISERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of the cDNA clone Bcl-like (HAICH29).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-NOV-1998 (first entry)
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              1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
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1998-414099/35.
                                                  144;
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                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                 Gentz RL,
                                                                                                                 365 AA;
                                              Conservative
                                                                                                                                      can also be used for detection and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorder; autoimmune disease; anti-infectious agent.
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97US-0034204.
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Pred. No.
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                                                        3.1e-76;
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The sequence represents the amino acid sequence of Bcl-Xl-DTR apoptosis-modifying fusion protein comprising Bcl-Xl sequence fused via a short linker to diphtheria toxin receptor binding domain (DTR). The functional apoptosis-modifying fusion protein is capable of binding a target cell and integrating into or crossing a cellular membrane of the target cell. comprising at least two domains, one of which targets the fusion protein to the target cell and another of which modifies an apoptotic response of the target cell. The fusion protein is useful for modifying (inhibiting
                                                                                                                                                                                          Novel fusion protein for modifying apoptosis in target cell and reducing apoptosis after transient ischaemic neuronal injury, has two domains which targets protein to a cell and modifies apoptotic response
                                                                                                                                                  Claim 4; Page 56-57; 65pp; English.
                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                         (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                          16-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diphtheria toxin receptor binding domain; DTR; neoplasm; tumour; hyper-proliferation; Alzheimer's disease; neurodegenerative disorder; transient ischaemic neuronal injury; stroke; spinal cord injury;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bcl-X1-DTR apoptosis-modifying fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bcl-X1-DTR; apoptosis; cancer; spinal muscular atrophy;
                                                                                                                                                                                                                                                                AAS00247
                                                                                                                                                                                                                                                                                                                                                             HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                             Liu X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium diptheriae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                         99US-0149220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
254..2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260..41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Linker amino acids, linking Bcl-xl to diphtheria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "10x histidine tag"
                                                                                                                                                                                                                                                                                                             Collier RJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "DTR, diphtheria toxin receptor binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Bcl-X1 amino acids 1 to 233"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          toxin receptor binding domain (DTR)"
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RESULT :
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or enhancing) apoptosis in a target cell, such as neuron, lymphocyte, cancer, neoplasm, macrophage, epithelial, stem, tumour or hyperproliferative cell or an adipocyte. It is also useful for reducing apoptosis in a subject after transient ischaemic neuronal injury, especially spinal cord injury. The fusion protein may be used to treat various diseases and injury conditions through inhibition or enhancement of apoptotic cellular response, including neurodegenerative disorders such as Alzheimer's disease, Huntington's disease, spinal muscular atrophy, stroke episodes and unregulated cell growth as in tumours and various cancers. The apoptosis-modifying fusion protein can be delivered celluse throughout the body and targeted to selective tissue and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                   BCL-XL; apoptosis; cell death; cancer; neurodegenerative disease; autoimmune disease; Parkinson disease; amylotrophic lateral sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human thymus BCL-XL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-AUG-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR68887 standard; Protein;
New poly-nucleotide encoding new poly-peptide(s) that modify apoptosis - and related vectors, recombinant cells and antibodies, useful in assay and for control of cell death in e.g. neuronal cells, lymphocytes and cancers
                                                                                                                                                                                                                                                                                              05-JAN-1995
                                                                                                                                                                     (ARCH-) ARCH DEV CORP. (UNMI ) UNIV MICHIGAN.
                                                                                                                                                                                                                                                             22-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGALVTVGAFFAS 192
                                                                                       N-PSDB; AAQ81698.
                                                                                                         WPI; 1995-052079/07.
                                                                                                                                        Boise LH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86 ngatahsssldarevipmaavkqalreagdefelryrrafsdltsqlhitpgtayqsfeq 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 D-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 RALVADFVGYKLRQKGY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ggwdtfvelygnnaaaesrkgqerfnrwfltgmtvagvvllgslfsrkaysaa 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93;
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93; Conservative
                                                                                                                                        Nunez G,
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                                                                                                                                        Thompson CB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 433.5; DB 2
Pred. No. 2.5e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----VCGAGP----GEGPAA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                  This protein may be expressed recombinantly, particularly with pcmV plasmids as vectors for expression in mammalian cell cultures. The protein has particular application in cancer cells (failure of programmed cell death (PCD)) or neurodegenerative and autoimmune diseases (premature PCD), e.g. Parkinson's disease, amylotrophic lateral sclerosis and multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 94; 127pp; English.
185 nggwdtfvelygnnaaaesrkgqerfnrwfltgmtvagvvllgsl 229
                                   141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                       125 qvvnelfrdgvnwgrivaffsfggalcvesvdkemqvlvsriaawmatylndhlepwige 184
                                                                                                             81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS 140
                                                                                                                                                   66 nga-tghsssldarevipmaavkqalreagdefelryrrafsdltsqlhitpgtayqsfe 124
                                                                                                                                                                                         29
                                                                                                                                                                                                                                                                11 RALVADFVGYKLRQKGY-----
                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                         {\tt 6\ relvvdflsyklsqkgyswsqfsdveenrteapegtesemetpsaingnpswhladspav}
                                                                                                                                                                                       CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
                                                                                               93;
                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  233 AA;
                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                          42.6%;
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                                                                                                                                                                                                                                                                                                                          Score 428.5; DB Pred. No. 4.1e-39
                                                                                                                                                                                                                                                                                                                                              DB 16; Length 233;
                                                                                                                                                                                                                                                                                                            57; Indels
                                                                                                                                                                                                                                                                          ----- 28
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Search completed: June 10, 2002, 10:25:47 Job time: 160 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MATPASAPDTRALVADFVGY.....LTGAVALGALVTVGAFFASK 193
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Bak protein - huma
gene bcl-xshort pr
cdn-2 protein - hu
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gene bcl-2 protein
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BCL-2 - rat (fragm
gene bcl-2 protein
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bcl-2-associated p
protein ced-9 [imp
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    bcl-2-associated
                       Bax-delta protein
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81.5	82.5	82.5	83	84.5	85	85	87	89	91.5	105	112	118	137.5	141	143
8.1	8.2	8.2	8.2	8.4	8.4	8.4	8.6	8.8	9.1	10.4	11.1	11.7	13.7	14.0	14.2
354	3432	1440	417	358	279	270	3433	185	301	172	350	175	143	255	177
N	٢	٢	N	ب	Ν	N	ب	ν	N	N	N	N	N	N	Ν
S52040	GNWVJE	GNWVJF	T39939	AJLCQB	в97381	AI2598	GNWVKV	B83217	T36534	I49449	A47476	139055	138921	JC7567	S54778
Gin 1.1 protein -	genome polyprotein	genome polyprotein	DNA binding protei	glutamateammonia	dihydrodipicolinat	dihydrodipicolinat	genome polyprotein	hypothetical prote	probable lipase/es	hemopoietic-specif	BCL2 homolog MCL1	Bc1-2 related - hu	bcl-2-associated p	Mcl-la protein - z	NR-13 protein - qu

## ALIGNMENTS

RESULT

bcl-x long - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 02-Uul-1996 #sequence\_revision 02-Jul-1996 #text\_change 16-Jul-1999 C;Accession: 149056; S52866 R;Fang, W; Rivard, J.J; Mueller, D.L.; Behrens, T.W. J. Immunol. 153, 4388-4398, 1994 A;Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes A;Reference number: I49055; MUID:95052604 A;Accession: I49056

A;Cross-references: EMBL:U10101; NID:g506647; PIDN:AAA82173.1; PID:g506648 R;Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M. submitted to the EMBL Data Library, November 1994 A;Description: IL-5 inhibits anti-IgM-induced apoptosis in an immature B ce A;Reference number: S52866 A;Accession: S52866

an immature B cell line

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A; Status: preliminary

A; Molecule type: mRNA A; Residues: 1-233 <RES>

A;Status: preliminary; translated from GB/EMBL/DDBJ

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Qγ
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A;Residues: 1-233 KRAD:
A;Cross-references: EMBL:X83574; NID:g695622; PIDN:CAA58557.1; PID:g695623
C;Superfamily: bcl transforming protein
                                     RESULT
B47537
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apoptosis regulator bcl-xL - human N; Alternate names: bcl-2-related protein
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Best Local Similarity
Matches 93; Conserv
                                                                                                                                                                                   185 NGGWDTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229
                                                                                                                                               141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                      81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS 140
                                                                                                                                                                                                                                                            66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124
                                                                                                                                                                                                                                                                                 29 CGAGPGEGPAAD------PLHQAMRAAGDEFETRERRTESDLAAQLHVTPGSAQQRFT 80
                                                                                                                                                                                                                                                                                                                                                                        11 RALVADFVGYKLRQKGY-----V 28
                                                                                                                                                                                                                                                                                                                                    6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV 65
                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   42.6%;
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Pred. No. 2.9
                                                                                                                                                                                                                                                                                                                                                                                                                 5; DB 2;
2.9e-32;
nes 57;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     53;
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A; Experimental source: embryonic; A; Note: smaller form due to splic C; Genetics:
                                                                                                                        A; Accession: S51762
A; Status: preliminary
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-125,189-233 <MI2>
A; Cross-references: EMBL: X82537; NID: 9607176;
A; Cross-references: EMBL: X82537; NID: 9607176;
  A; Introns: 125/3
C; Superfamily: b;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 02-Mar-2001
C;Accession: S51761; S51762
R;Michaelidis, T.M.
                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X82537; NID:g607176; PIDN:CAA57886.1; PID:g607177 A;Experimental source: embryonic; brain
                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, November 1994 A; Reference number: S51761
                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-233 <MIC>
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C;Superfamily: bcl transforming protein
C;Keywords: alternative splicing; apoptosis
F;1-233/Product: apoptosis regulator bcl-xL #status predicted <MAT>
F;1-125,189-233/Product: apoptosis regulator bcl-xS #status predicted <MA2>
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A; Residues: 1-69, 'G', 71-125, 189-233 <B02>
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A; Residues: 1-233 <BOI>
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A;Title: bcl-x, a bcl-2_related gene that functions as a dominant regulator of apoptoti
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C;Species: Homo sapiens (man)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Jul-1999
C;Accession: B47537; C47537
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 RALVADFVGYKLRQKGY------39
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bcl transforming protein
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40.6%; Pred. No. 2.9
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2.9e-32;
ches 59; Indels 51
                                                                                                                                      PIDN:CAA57887.1; PID:g607178
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R;Cazals-Hatem, D.L.; Louie, R;Cazals-Hatem, D.L.; Louie, R;Cazals-Hatem, Riophys. Acta 1132,
                                           C; Accession: S24390
                                                           transforming protein (Bc1-2) homolog - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
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C;Keywords: mitochondrion; transforming protein; transmembrane protein
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c;Species: Gallus gallus (chicken)
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 23-Feb-1997
C;Accession: A37332; S35453
C;Accession: A37332; S35453
R;Eguchi, Y; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expressi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics:
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A; Residues: 1-233 < EGU>
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                                                                                                                                                                                                                                                           145 AEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 LVADFVGYKLRQKGY-------
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                                                                                                                                                                                                                                                                                                                                                ELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGW 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87;
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38.08;
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D.C.; Tanaka,
109-113, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32;
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Pred. No. 8.4e-32;
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Pred. No. 6.8e-32
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                    S.; Reed, J.C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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A;Cross-references: EMBL:Z11961; NID:g62969; PIDN:CAA78018.1; PID:g62970 C;Superfamily: bcl transforming protein C;Keywords: mitochondrion; transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S24390
A; Status: preliminary
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C;Date: 31-Dec-1988 #sequence_revision 07-Jun-1996 #text_change 15-Oct-1999
C;Accession: C37332; A29409; S02452; A24428; A27622; B27622
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A; Residues: 1-232 <CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Note: this report is a correction R;Tsujimoto, Y.; Croce, C.M. Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986 A;Title: Analysis of the structure, transcripts, and protein products of bcl-2, the gene A;Reference number: A29409; MUID:86259760 A;Accession: A29409
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Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transforming protein bcl-2, splice form alpha - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-95,'A',97-109,'G',111-236,'S',238-239 <TSU>
A; Cross-references: GB:M13994; NID:g179366; PIDN:AAA51813.1; PID:g179367
A; Note: this sequence has been corrected in reference A37332
A; Note: this sequence has been corrected in reference A37332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-239 <EGU>
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A;Molecule type: mRNA
A;Residues: 1-58,'T',60-116,'R',118-239 <CLE>
A;Cross-references: GB:M14745; NID:g179370; PIDN:AAA35591.1; PID:g179371
A;Cross-references: GB:M14745; NID:g179370; PIDN:g179371
A;Cross-references: GB:M14745; NID:g179370; PIDN:AAA35591.1; PID:g179371
A;Cross-references: GB:M14745; NID:g179370; PIDN:AAA35591.1; PID:g179370; PID:g179370;
                                                                                                                                                                                                                                                                                                                                           R;Cleary, M.L.; Smith, S.D.; Sklar, J. Cell 47, 19-28, 1986
A;Title: Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Alternative promoters and exons, somatic mutation and deregulation of the Bcl-A;Reference number: S02452; MUID:88196071
A;Accession: S02452
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                                                                                                                                                                                                                                                                                  A; Reference number: A24428; MUID:87002488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130 LFRDGVNWVRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGWD 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLVRCPRLRGCAAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTATGRFVAVVEE 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDE 85
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A;Title: Consequences of the t(14;18) chromosomal translocation in follicular lymphom A;Reference number: A27622; MUID:88217344
A;Accession: A27622
A;Molecule type: mRNA
A;Residues: 1-58,'T',60-239 <HUA>
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A;Map position: 18q21.3-18q21.3
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A; Residues: 1-6,'S',8-58,'T',60-128,'C',130-239 <HUA2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C;Accession: 167432
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                                                                                                                                                                                                                                                                                                                               R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L. Endocrinology 136, 232-241, 1995
Endocrinology 136, 232-241, 1995
A;Title: Expression of members of the bcl-2 gene family in onstitutive bcl-2 and bcl-xlong messenger ribonucleic acid A;Reference number: I53295; MUID:95129487
A;Accession: I67432
                                                                                                                                                                                                           A; Residues: 1-236 <RES>
A; Cross-references: EMBL: U34964; NID: g1
C; Superfamily: bcl transforming protein
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                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                          Query Match
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    rat (fragment)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 DTRALVADFVGYKLRQKGYVCGAG------PGE-----PGE-----
10 DNREIVMKYIHYKLSQRGYEWDTGDEDSAPLRRAPTPGIFSFQPESNRTPAVHRDTAART 69
                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPLQTPAAPGAAAGPALSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARGR 129
                                             DTRALVADEVGYKLRQKGY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87;
                                                                                               84;
                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                  Conservative
                                                                                                                                                                                                                                    EMBL: U34964; NID: g1004378; PIDN: AAA77687.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.0%; Score 412.5;
37.0%; Pred. No. 9e-
                                                                                                                      40.9%;
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                                                                                                  34; Mismatches
                                                                                                                        Score 412; DB 2;
Pred. No. 9.9e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9e-31;
                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59;
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                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  the immature rat ovary:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55;
                                                                                                         52;
                                                                                                                                                                                                                                                 PID:g1004379
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-----VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81

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A;Cross-references: GB:L31532; GB:M16506; NID:g468336; PIDN:AAA37282.1; PID:g387109 R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y. Nucleic Acids Res. 20, 4187-4192, 1992 A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a A;Reference number: A37332; MUID:92375724 A;A;A;Ccession: E37332
                  A; Molecule type: DNA
A; Residues: 1-33,'E',34-220,'AL',223-236 <EGU>
C; Genetics:
A; Gene: BCL2
                                                                                        A: Status: preliminary; nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                             R;Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.
Cell 49, 455-463, 1987
A;Title: Molecular analysis of mbcl-2: structure and expression of the murine gene homo
                                                                                                                                                                                                                                                                                                                                                                                            C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1999
C:Accession: A25960; E37332
                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-236 < NEG>
                                                                                                                                                                                                                                                                                                    A; Accession: A25960
                                                                                                                                                                                                                                                                                                                        A; Reference number: A90893;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene bc1-2 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-May_1998 #sequence_revision 29-May-1998 #text_change 16-Ju1-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:L14680; NID:g408946; PIDN:AAA53662.1; PID:g408947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-236 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene 140, 291-292, 1994
A;Title: Cloning and sequencing of a cDNA encoding the A;Reference number: I53744; MUID:94193015
A;Accession: I53744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C. Gene 140, 291-292, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 VVEELFRDGVNWGRIVAFFEFGGVMCVGSVNREMSPLVDNIALWMTEYLNRHLHTWIQDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141 | :|| : || || || || : || || || :||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 SPLRPLVANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 DNREIVMKYIHYKLSQRGYEWDTGDEDSAPLRAAPTPGIFSFQPESNRTPAVHRDTAART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 40.4%;
Local Similarity 35.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 DTRALVADFVGYKLRQKGY----------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bc1-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGWDAFVELYG----PSMRPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
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                                                                                                                                                                                                                                                                                                                      MUID:87187643
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Pred. No. 2
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.9e-30;
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                                                                                           not compared with conceptual
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                                                                                             tra
                      B-cell lymphoma 2 protein - Chinese hamster C;Speckes: Cricetulus griseus (Chinese hams: C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2006)
                                                                                                                  JC7383
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R; Tomicic, M.T.; Christmann, M.; Kaina,
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R:Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
Endocrinology 136, 232-241, 1995
A:Title: Expression of members of the bcl-2 gene family in
onstitutive bcl-2 and bcl-xlong messenger ribonucleic acid
A:Reference number: 153295; MUID:95129487
A:Accession: 167431
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A; Residues: 1-233 < RES>
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C;Superfamily: bcl transforming protein
C;Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane
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                                                                                                                                                                                        185 NGGWDTFVDLYGNNTAPESRKGQERFNRWFLTGMTVAGVVLLGSL
                                                                                                                                                                                                                                      141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190
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89; Conserv
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37.1%;
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Pred. No. 4.8e-30;
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Pred. No. 3.6e-30;
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                                         hamster)
17-Nov-2000
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C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                  125 QVVNELFRDGVNWGRIVASSSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE 184
                                                                                                                                                                                                                                                                                                                                                                                         81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 NGA-TGHSSSLDAREVLPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTVYQSFE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 CGAGPGEGPAAD------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEPERETPSAINGNPSWHLADSPAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----EGPAADP----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL: U34963; NID: g1004376; PIDN: AAA77686.1; PID: g1004377
#text_change 08-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 236;
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Biochem. Biophys. Res. Commun. 275, 899-903, 2000
A;Title: Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein.
A;Reference number: JC7383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: bcl-2
C;Superfamily: bcl transforming pro
C;Keywords: B-cell lymphoma; ovary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Comment: This protein has anti-apoptotic function, and supports cell survival.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
A47537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-236 <TOM>
A; Cross-references: GB:AJ271720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Contents: Ovary
A; Accession: JC7383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-190 <BOI>
A;Cross-references: GB:Z23110; GB:L20120; NID:g510898; PIDN:CAA80657.1; PID:g510899
C;Superfamily: bcl transforming protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R:Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.; Cell 74, 597-608, 1993
A;Title: bol-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       apoptosis regulator bcl-x - chicken
C;Species: Gallus gallus (chicken)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 16-Jul-1999
C;Accession: A47537
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match 40.0%; Score 403; DB 2; Length 236; Local Similarity 35.3%; Pred. No. 6.7e-30; nes 82; Conservative 34; Mismatches 64; Indels
     186 R-TAL
                                                  146 EFTAL 150
                                                                                          126 LFHDGVNWGRIVAFFSFGGALCVESVDKEMRVLVGRIVSWMTTYLTDHLDPWIQENGGWV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 DNREIVMKYIHYKLSQRGYEWDVGDVDAAPLGAAPTPGIFSFQPESNPTPAVHRDMAART
                                                                                                                                                                                         66 VHRSSLEVHEIVRASDVRQALRDAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNE 125
                                                                                                                                                                                                                                                                                                                                     11 RALVADFVGYKLRQKGY-----
                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPLRPIVATTGPTLSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                                                                                                                                         LFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWA 145
                                                                                                                                                                                                                                      -----AADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDE 85
                                                                                                                                                                                                                                                                                        RELVIDEVSYKLSORGHCWSELEEEDENRTDTAAEAEMDSVLNGSPSWHPPAGHVVNGAT 65
                                                                                                                                                                                                                                                                                                                                                                                     81;
       189
                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           37.5%; Score 378; DB 2; Length 190; 43.8%; Pred. No. 1.1e-27;
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J. Immunol. 153, 4388-4398, 1994
A;Title: Cloning and molecular characterization of mouse A;Reference number: I49055; MUID:95052604
A;Accession: I49057
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C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: bcl-x-long C; Superfamily: bcl transforming protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-214 <RES>
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                                                                                                                                                                                                                                                                                                                                                                  R;Ban, J.; Eckhart, L.; Weninger, W.; Mildner, M.; Tschachler, E. Biochem. Biophys. Res. Commun. 248, 147-152, 1998 A;Title: Identification of a human cDNA encoding a novel bcl-x isoform. A;Reference number: JE0203; MUID:98340865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             apoptosis regulator bcl-x isoform - N; Alternate names: h-bcl-xbeta
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JE0203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:U10102; NID:g506649; PIDN:AAA82174.1; PID:g506650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 16-Jul-1999
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                                                                                                                                                                                                                       A; Map position: 20 C; Superfamily: bcl transforming protein
                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-227 <BAN>
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QY
                                        B
                                                                             Qy
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                                                                                                                                                                                                                                                                  A;Gene: bcl-x
                                                                                                                                                                                                                                                                                       C;Genetics
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                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29
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                                                                               11 RALVADFVGYKLRQKGY-----
  29 CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT
                                                                                                                                         Local Similarity
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                                        RELYVDFLSYKLSOKGYSWSOFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV
                                                                                                                          82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                          Conservative
                                                                                                                                           37.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                          18;
                                                                                                                        Score 375.5; DB 2
Pred. No. 2.3e-27;
8; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------ 28
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1.4e-27;
                                                                                                                                                                   DB 2;
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                                                                                                                              51; Gaps
                                                                                        ---- 28
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Search completed: June 10, 2002, 10:26:22 Job time: 170 sec
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C.Species: Gallus gallus (chicken)
C.Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 24-Apr-1998
C.Accession: B37332; S35452
R.Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie A; Reference number: A37332; MUID:92375724
A;Status: nucleic acid sequence not shown
A, Accession: B37332
A;Status: nucleic acid sequence not shown
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A; Residues: 1-216 <EGU>
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B37332
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 35.4%; Score 356; DB 2; Length 216; Best Local Similarity 38.4%; Pred. No. 1.4e-25; Matches 71; Conservative 21; Mismatches 49; Indels 44; Gaps
                                                                                                       190 VRACA 194
                                                                                                                                                                                 130 ELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGW 189
                                                                                                                                                    145 AEFTA 149
                                                                                                                                                                                                                 85 ELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGW 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 NGGWVRTKPLVCPFSLASGOR 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQE 184
                                                                                                                                                                                                                                                                     70 AASEVPPAEGLRPAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTAHGRFVAVVE 129
                                                                                                                                                                                                                                                                                                  10 DNREIVLKYIHYKLSQRGYDWAAGEDRPPVPPAPAPAAAPAAVAAAGASSHHRPEPPGSA 69
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Best Local
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                             ROSS A.J., Waymire K.G., MOSS J.E., Parlow A.F., Skinner M.K.,
"Testicular degeneration in Bclw-deficient mice.";
Nat. Genet. 18:251-256(1998).
-!- FUNCTION: PROMOTES CELL SURVIVAL.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MYELOID CELL LINES AND IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50062; BCL2_FAMILY PROSITE; PS01080; BH1; 1. PROSITE; PS01258; BH2; 1. PROSITE; PS01260; BH4 1; 1. PROSITE; PS50063; BH4_2; 1.
                                                                                                                                                                                                              MEDLINE=96358615; PubMed=8761287; Gibson L., Holmgreen S.P., Huang D.C., Bernard O., Copeland N.G., Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.; "bcl-w, a novel member of the bcl-2 family, promotes cell survival.";
                                                                                                                                              STRAIN=C57BL/10J;
MEDLINE=98160183; PubMed=9500547;
                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                         Oncogene 13:665-675(1996).
                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                               Apoptosis regulator Bcl-W. BCL2L2 OR BCLW.
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
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SEQUENCE
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Pfam; PF02180; BH4; 1.
SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
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 AND SALIVARY GLAND.

DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
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193 AA;
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104 BJ
151 BI
; 20774 MW;
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Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                       В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 191;
                                                                                                                                                     AR1_XENLA
Q91827;
01-NOV-1997
                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                       Apoptosis regulator R1 (XR1) (Fragment).
TISSUE=Head;
          SEQUENCE FROM N.A.
                                      Xenopodinae; Xen
NCBI_TaxID=8355;
                                                                 Amphibia; Batrachia; Anura;
                                                                                                                      01-NOV-1997 (Rel. 35, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation
                                                                                            Xenopus laevis (African clawed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00452; Bcl-2; Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                      181 GALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apoptosis.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002475; BCL2_family.
InterPro; IPR003093; BH4.
InterPro; IPR0007112; Bcl_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:108052;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U59746; AAB09056.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               issp;
                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                             61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEDLVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                                                                                                                        QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
                                                                                                                                                                                                                                                        GALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                     QVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                    MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                                                                                                                                                                                                                                                                              FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q07817; 1MAZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF030769; AAB86430.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS50062; BCL2_FAMILY; 1.
PS01080; BH1; 1.
PS01258; BH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS01260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193 AA;
                                                                                                                                                       (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                     Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85
9
                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  вн2; 1.
вн4_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bc1212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 B
104 B
151 B
: 20790 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BH4_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.3%;
99.0%;
                                                             Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1000; DB 1;
Pred. No. 1e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BH4.
BH1.
BH2.
; 36CA185F5945DFB4 CRC64;
                                                                                                                                                                                  PRT;
                                                                                              frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                      update)
                                                                                                                                                                                228 AA.
                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
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SO TITES NO DE RESERVA DE RESERVA
  RESULT 4
BCLX_CHICK_ID 107816
AC Q07816
DT 01-FEB
DT 16-OCT
DE Apopto
GN BCL2L1
OS Gallus
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell-survival genes.";
Gene 158:171-179(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cruz-Reyes J., Tata J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95331613; PubMed=7607538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS01258; BH2; 1.
PROSITE; PS50062; BCL2_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
Apoptosis regulator Bcl-X.
BCL2L1 OR BCLX OR BCL-X.
Gallus gallus (Chicken).
                                                                                 007816; 098908;
01-FEB-1995 (Rel. 31, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                               BCLX_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130
                                                                                                                                                                                                                                                                                                                                       225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Membrane-bound (Potential).

DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE BRAIN OF MID-METAMORPHOSIC TO POST-METAMORPHOSIC TADPOLES AND ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: COULD BE THE HOMOLOG OF MAMMALIAN BCL-W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through
sen the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLH 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRALVEDLVRYKLCORSLV---PEPSGAASCALHSAMRAAGDEFEERFROAFSEISTOIH 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pro; IPR000712; Bcl_2.
PF00452; Bcl-2; 1.
PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  x82462; CAA57845.1; -.
Q07817; 1MAZ.
Pro; IPR002475; BCL2_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAF
                                                                                                                                                                                                                                                                                                                                       FASK 228
                                                                                                                                                                                                                                                                                                                                                                                            FASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VTPGTAYARFAEVAGSLFQGGVNWGRIVAFFVFGAALCAESVNKEMSPLLPRIQDWMVTY 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                LETNLRDWIQSNGGWNGFLTLYGDGAIEEARRQREGNWASLKTVLTGAVALGALMTVGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS01080; BH1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            characterization and expression of two Xenopus bcl-2-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR003093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25068 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 646.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C499D449A585F8A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No. 5.7e-51
                                                                                                                                                                                                     229
                                                                                                                                                                                                     A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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Vilagrasa X., Mezquita C., Mezquita J.;
"Differential expression of bcl-2 and bcl-x during chicken spermatogenesis.;
Mol. Reprod. Dev. 47:26-29(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (LONG FORM).
STRAIN=HUBBARD WHITE MOUNTAIN; TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic cell death.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boise L.H., Gonzalez-Garcia M.,
Turka L.A., Mao X., Nunez G., T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (SHORT FORM).
MEDLINE=93364977; PubMed=8358789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus.
NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z23110; CAA80657.1; -. EMBL; U26645; AAB07677.1; -. PIR; A47537; A47537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97264485; PubMed=9110311;
                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
PROSITE; PS50062; BCL2_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
SEQUENCE
                                                                                                                                                                                            Apoptosis;
                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                          PROSITE
                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003093; BH4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute.
                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR000712; Bcl_2.
                                                       VARSPLIC
                                                                                    TRANSMEM
                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-APOPTOTIC ACTIVITY (BY SIMILARITY).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENVELOPE (BY SIMILARITY).

ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ORGANS WITH LYMPHOID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPTOOL DEV. 47:26-29(1997).
FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE ISOFORM PROMOTES APOPTOSIS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISOFORM PROMOTES APOPTOSIS (BY SIMILARITY).
SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEVELOPMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74:597-608(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF02180; BH4; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P53563; 1AF3
                                                                                                                                                                                                                                                                                                    PS01080; BH1;
PS01258; BH2;
PS01259; BH3;
                                                                                                                                                                                                                                                PS01260; BH4_1;
PS50063; BH4_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR002475; BCL2_family.
                                                                                                                                                                                                                            Transmembrane;
  229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bcl-2;
                                                            24
96
144
191
223
  25733
     MW.
                                                                                                                                                                                                                            Alternative splicing
  BH1.
BH2.

POTENTIAL.

POTENTIAL.

ERFVDLYGNNAAAELRKGQETENKWLLTGATVAGVLLLGSL
LSRK -> VRTALP (IN SHORT ISOFORM).

; A97D3A4D04C0E9DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thompson C.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Postema C.E., Ding L., Lindsten T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                  modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                      the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
                                                                                                                                                        between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G. "Expression of apoptosis-associated genes in hibernating myocardium of pig.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Potent inhibitor of cell death. Inhibits a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apoptosis regulator Bcl-x.
BCL2L1 OR BLC2L OR BCLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BCLX_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        146 EFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 LFHDGVNWGRIVAFFSFGGALCVESVDKEMRVLVGRIVSWMTTYLTDHLDPWIQENGGWE 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 VHRSSLEVHEIVRASDVRQALRDAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 RALVADFVGYKLRQKGY-----------VCGAGPGEGP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                      apoptotic activity (By similarity).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                DOMAIN: The BH4 domain is required for anti-apoptotic activity. The BH1 and BH2 domains are required for both heterodimerization with other Bc12 family members and for repression of cell death. PTM: Proteolytically cleaved by caspases during apoptosis (By Similarity). The cleaved protein, lacking the BH4 domain, has protein.
                                                                                                                                                                                                                                                                                                                                                                                                            SÜBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 similarity). Heterodimerization with BAX does not seem to be required for anti-apoptotic activity (By similarity). SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR ENVELOPE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            caspases (By similarity). Appears to regulate cell death by blocking the volatage-dependent anion channnel (VDAC) by binding to it and preventing the release of the caspase activator, cytochrome c, from the mitochondrial membrane.

SUBUNIT: Bcl-x(L) forms heterodimers with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G
  Q07817; 1MAZ
                    AJ001203; CAA04597.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RFVDLYGNNA---AAELRKGQETFNKWLLTGATVAGVLL-LGSLLSRK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RELVIDFVSYKLSORGHCWSELEEEDENRTDTAAEAEMDSVLNGSPSWHPPAGHVVNGAT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42.9%; Score 432.5; DB 1; 41.7%; Pred. No. 8.4e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schulz R., Heusch G., Darmer D.; genes in hibernating and stunned
                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 AA.
                                                                                                        There are no restrictions on ong as its content is in no
                                                                                    Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 229;
                                                                                        bУ
                                                                                        and
                                                                                        for
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                                                                                        commercia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Ву
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                                                                                                                                                                                                                                                                                                                                                                   BCLX_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                           Boise L.H., Gonzalez-Garcia M., Postema C.E.
Turka L.A., Mao X., Nunez G., Thompson C.B.,
"bcl-x, a bcl-z-related gene that functions
of apoptotic cell death.";
                                                                                                                                                                                                                                                                                         BCLX_HUMAN STANDARD; PRT; 2
Q07817; Q92976;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence up
01-MAR-2002 (Rel. 41, Last annotation
        Sedlak T.W., Oltvai Z.N., Yang E., Wang K.,
                       MUTAGENESIS OF GLY-138, AND HETERODIMERIZATION MEDLINE=95372373; PubMed=7644501;
                                                             Inohara N., Ohta S.;
Submitted (OCT-1996) to
                                                                                                                  Cell
Korsmeyer S.J.;
                                                                                    SEQUENCE FROM N.A. (ISOFORM BETA).
                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                               MEDLINE=93364977; PubMed=8358789;
                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
                                                                                                                                                                                                                                                                      Apoptosis regulator Bcl-x.
BCL2L1 OR BCL2L OR BCLX.
                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002475; BCL2_family.
InterPro; IPR003095; BH4.
InterPro; IPR000712; Bc1_2.
Pfam; PF00452; Bc1-2; 1.
Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00337; BCL; 1. SMART; SM00265; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                    185
                                                                                                                                                                                                                                                                                                                                                                                                                                        141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 RALVADFVGYKLRQKGY-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 RELVVDFLSYKLSQKGYSWSQFTDVEENRTEAPEGTESEAETPSAINGNPSWHLADSPAV
                                                                                                                 74:597-608(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                NGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTLAGVVLLGSL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVLNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS01259; BH3; 1.
PS01260; BH4_1; 1.
PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS50062; BCL2_FAMILY; 1.
PS01080; BH1; 1.
PS01258; BH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210
233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86
129
180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148
195
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100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26061 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42.9%; Score 431.5; DB 41.8%; Pred. No. 1.1e-31
                                                           the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21; Mismatches
                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                               Postema C.E., Ding L., Lindsten T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18BF6FA0441912B2 CRC64;
                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                   233 AA
                                                                                                                                                                                                                                                                                                update)
         Boise L.H., Thompson C.B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                        as a
                                                                                                                                      dominant regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----- 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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cell
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[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLEAVAGE BY CASPASES, AND MUTAGENESIS OF MEDILINE-98118550; PubMed=9435230; Clem R.J., Cheng E.H.-Y., Karp C.L., Kirs Takahashi A., Kastan M.B., Griffin D.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structure of Bcl-xL-Bak peptide complex: recognition between regulators of apoptosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eberstadt M., Yoon H.S.,
Thompson C.B., Fesik S.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRUCTURE BY NMR OF 1-209
MEDLINE=97172562; PubMed=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cheng E.H.-Y., Levine B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ng S.L., Fesik S.W.;
"X-ray and NMR structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND STRUCTURE BY NMR OF MEDLINE-96256675; PubMed-8692274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sattler M., Liang H., Nettesheim D., Meadows R.P.,
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[7]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUTAGENESIS
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                   between
                                                                                                                                                                                                     This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Modulation of cell death bx Bcl-xL through caspase interaction.";
Proc. Natl. Acad. Sci. U.S.A. 95:554-559(1998).
-i- FUNCTION: Potent inhibitor of cell death. Inhibits activation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hardwick J.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALTERNATIVE PRODUCTS: 3 ISOFORMS; BCL-X(L) (SHOWN HERE), BCL-X(S) AND BCL-X(BETA); ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: BCL-X(S) IS EXPRESSED AT HIGH LEVELS IN CELLS
THAT UNDERGO A HIGH RATE OF TURNOVER, SUCH AS DEVELOPING
LYMPHOCYTES. IN CONTRAST, BCL-X(L) IS FOUND IN TISSUES CONTAINING
LYMPHOCYTES. IN CONTRAST, BCL-X(L) IS FOUND IN TISSUES CONTAINING
LONG-LIVED POSTMITOTIC CELLS, SUCH AS ADULT BRAIN.

DOMAIN: The BH4 domain is required for anti-apoptotic activity.

The BH1 and BH2 domains are required for both heterodimerization.
                                                                                                                                                                                                                                                                                              SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  apoptotic activity.
SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Bcl-x(L) forms het
                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    with other Bcl2 family members and for repression of cell death. PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heterodimerization with BAX does not seem to be required for anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to it and preventing the release of the caspase activator cytochrome c, from the mitochondrial membrane. The Bcl-\mathbf{x}(:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            caspases (By similarity). Appears to regulate cell death by blocking the volatage-dependent anion channnel (VDAC) by binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENVELOPE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Natl. Acad. Sci. U.S.A. 92:7834-7838(1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AND BH2 DOMAINS.
PubMed=8596636;
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                                                                                                                                                                                                                                                                   TO THE BCL-2 FAMILY.
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SMART; SM00265; BH4; 1
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3D-structure.
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185
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1LXL; 21-APR-97
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                                                                                                                                                NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124
NGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
                                   SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                         QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQE
                                                                                            QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAXLETRLADWIHS 140
                                                                                                                                                                                                                           RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV
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Z23115; CAA80661.1;
U72398; AAB17354.1;
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PS01080; BH1;
PS01258; BH2;
PS01259; BH3;
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BH4_2; 1.
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41.3%;
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                                                                                                                                                                                                                                                                                                    22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLEAVAGE BY CASPASE-1.
MISSING (IN ISOFORM BCL-X(S)).
DTFVELYGNNAAAESERGQERENRWFLTGMTVAGVVLLGSL
FSRK -> VRTKPLVCDFSLASGQRSFTALLLYLFLLCWVI
                                                                                                                                                                                                                                                                                                                                                                                                                D->A: NO EFECT ON CASPASE-1 CLEAVAGE G -> A (IN REF. 1; CAA80661).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D->A: NO EFECT ON CASPASE-1 CLEAVAGE
D->A: NO EFECT ON CASPASE-1 CLEAVAGE
                                                                                                                                                                                                                                                                                                                     Score 428.5;
Pred. No. 2e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CASPASE - 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D->A:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY ABOUT HALF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WD->GA: REDUCES ANTI-APOPTOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRI->ELN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VNW->AIL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRD->VRA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGDVDS
                                                                                                                                                                                                                                                                                                                                                                                                E09D3CDD851AE9BE CRC64;
                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLEAVAGE BY CASPASE-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            splicing; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HETERODIMERIZATION WITH BAX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOSS OF ANTI-APOPTOTIC
                                                                                                                                                                                                                                                                                                                       2e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOSS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NO HETERODIMERIZATION WITH BAX
                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-APOPTOTIC
                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                       53;
                                                                                                                                                                                                                                                                  ----- V 28
                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                            65
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RESULT 7
BCLX\_MOUSE

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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-97289584; PubMed-9144489;
Grillot D.A., Gonzalez-Garcia M., Ekhterae D., Duan L.,
Ohta S., Seldin M.F., Nunez G;
Ohta S., Seldin M.F., Contact Torion analysis, and chi
                                                                                                                                                                                                                         -
                                                                                                                                                                                                                                                                                                                                                                                                                                           -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genomic organization, promoter region analysis, and ch
localization of the mouse bcl-x gene.";
J. Immunol. 158:4750-4757(1997).
-i- FUNCTION: Potent inhibitor of cell death. Inhibits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6 X CBA; TISSUE=Thymus; MEDLINE=98051053; PubMed=9390687; Yang X.-F., Weber G.F., Cantor H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS X(L); X(S) TISSUE-Pre-B cell; TISSUE-Pre-B cell; MEDLINE-95052604; PubMed-7963517; Fang W., Rivard J.J., Mueller D.L., Behr Cloning and molecular characterization tempology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thompson C.B., Nunez G.;
"bcl-XL is the major bcl-x mRNA form edevelopment and its product localizes
Development 120:3033-3042(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BCLX_MOUSE STANDARD;
BCLX_MOUSE STANDARD;
Q64373; Q60657; Q60658; Q61338;
Q1-NOV-1997 (Rel. 35, Last seque
Q1-MOV-1997 (Rel. 35, Last seque
Q1-MAR-2002 (Rel. 41, Last annot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95331139; PubMed=7607090;
Gonzalez-García M., Perez-Ballestero
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             apoptosis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6; TISSUE=Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS X(L) AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kamesaki H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-2A4B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apoptosis regulator Bcl-x.
BCL2L1 OR BCL2L OR BCLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lymphocytes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mmunity 7:629-639(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             novel Bcl-x isoform connected to the T cell receptor regulates optosis in T cells.";
        POSTNATAL TISSUES, WHEREAS POSTNATAL TISSUES.

DOMAIN: The BH4 domain is 1
The BH1 and BH2 domains are
                                                                                                                                                                                                                                                                                      isoform promotes apoptosis.

SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (
similarity). Heterodimerization with BAX does not seem to be 
required for anti-apoptotic activity (By similarity).

SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR 
ENVELOPE FOR BCL-X(L). CYTOPLASMIC FOR BCL-X(DELTA-TM).

ALTERNATIVE PRODUCTS: 4 ISOFORMS; BCX-X(L) (SHOWN HERE), BCL-X

ALTERNATIVE PRODUCTS: 4 ISOFORMS; BCX-X(L) (SHOWN HERE), BCL-X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunol. 153:4388-4398(1994).
                                                                                                              DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          caspases (By similarity). Appears to regulate cell death by blocking the volatage-dependent anion channnel (VDAC) by binding to it and preventing the release of the caspase activator,
                                                                                                                                                                                                                                                                        BCL-X(BETA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytochrome c, from the mitochondrial membrane. The
                                                                                                                                                               IN, THYMUS, BONE MARROW, AND KIDNEY. BCL-X(L) A EXPRESSION IS ENHANCED IN B AND T LYMPHOCYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H., Michaud G.Y., 7 (MAR-1995) to the
                                                                                                                                                                                     SPECIFICITY: WIDELY EXPRESSED, WITH HIGHEST LEVELS IN THE THYMUS, BONE MARROW, AND KIDNEY. BCL-\chi(L) AND BCL-\chi(DELTA-THYMUS, BONE MARROW, AND KIDNEY. BCL-<math>\chi(L)
                                                                                                                                                                                                                                                                        AND BCL-X(DELTA-TM); ARE PRODUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ISOFORM X(BETA)).
domain is required for anti-apoptotic activity domains are required for both heterodimerization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence
                                                                                                              BCL-X(BETA) IS EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Takatsu K., Okuma M.;
e EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                               BCL-X(L)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X(S) AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Behrens
tion of m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expressed during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X(BETA)).
                                                                                     \mathbf{SI}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mitochondria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ding L., Duan L., Boise
                                                                                     PREDOMINANTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s T.W.;
mouse bcl-x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X(DELTA-TM))
                                                                                                              H
                                                                                                                                                                                                                                                                        BY ALTERNATIVE
                                                                                                              BOTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome
                                                                                                                                                                     THAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bcl-x(S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          activation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ĺn
                                                                                     FOUND
                                                                                                              EMBRYONAL
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                                                                                                                                                                  HAVE
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other Bcl2

family members

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for

repression

both heterodimerization

cell death

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:88139; Bc121.
InterPro; IPR002475; BCL2_family.
InterPro; IPR003093; BH4.
InterPro; IPR000712; Bc1_2.
Pfam; PF00452; Bc1-2; 1.
Pfam; PF02180; BH4; 1.
SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apoptosis;
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           VARSPLIC
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- PTM: Proteolytically cleaved by caspases during apoptosis similarity). The cleaved protein, lacking the BH4 domain, apoptotic activity (By similarity).
-!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
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    125
                                           81
                                                                                      66
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                                                                                                                                                                                                                   11 RALVADFVGYKLRQKGY-----------
                                                                                                                                                                            6
                      QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWWYAYLETRLADWIHS
QVVNELERDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE
                                                                                                                            CGAGPGEGPAAD------PLHQAMRAAGDEFETRFRTFSDLAAQLHVTPGSAQQRFT
                                                                                                                                                                        RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV
                                                                                      NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE
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U51279;
U78031;
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L35049;
L35048;
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U10101;
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                                                                                                                                                                                                                                                                  93;
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3; PS01080; BH1; 1.

5; PS01258; BH2; 1.

5; PS01259; BH3; 1.

6; PS01260; BH4_L; 1.

6; PS50063; BH4_L; 1.
                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                           233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86
129
180
180
210
126
189
                                                                                                                                                                                                                                                                Conservative
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AAA51039.1;
AAA51040.1;
AAA82174.1;
AAA82173.1;
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148
195
226
188
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                                                                                                                                                                                                                                                                                     42.6%;
                                                                                                                                                                                                                                                                                                                                                                           MW;
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                                                                                                                                                                                                                                                                22; Mismatches
                                                                                                                                                                                                                                                                                  Score 428.5; DB Pred. No. 2e-31;
                                                                                                                                                                                                                                                                                                                                                                         X(DELTA-TM)).
; 24D2AC79887E072E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
MISSING (I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISSING (IN ISOFORM BCL-X(S)).
DTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSI
                                                                                                                                                                                                                                                                                                                                                                                                                                      BCL-X(BETA)).
LYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSLFSRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FSRK -> VRTTPLVCPPLACVSLLCEHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         splicing; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                         CRC64
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has
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141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183

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DETECTABLE LEVEL OF BCL-X(S). DOMAIN: The BH4 domain is required for anti-apoptotic activity. The BH1 and BH2 domains are required for both heterodimerization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P53563; Q62678; P70614; P70613; Q62836; Q64087; Q64128; 
01-QCT-1996 (Rel. 34, Created) 
01-NOV-1997 (Rel. 35, Last sequence update) 
16-QCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95129487; PubMed=7828536; Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.; Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.; "Expression of members of the bcl-2 gene family in the immature rat ovary: equine chorionic gonadotropin mediated inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apoptosis regulator Bcl-x.
BCL2L1 OR BLC2L OR BCLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BCLX_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shiraiwa N., Inohara N., Okada S., Yuzaki M., Shoji S.-I., Ol
"An additional form of rat Bcl-x, Bcl-xbeta, generated by an
unspliced RNA, promotes apoptosis in promyeloid cells.";
J. Biol. Chem. 271:13258-13265(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wesselingh S.L., David G.L., Choi S., Veliuona M., Submitted (JUN-1995) to the EMBL/GenBank/DDBJ data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain;
Michaelidis T.M.;
                                                                                                                                                                                                                                                                                                                                                                the Bcl-2 protein family ;
J. Biol. Chem. 272:27886-27892(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-SPRAGUE-DAWLEY; TISSUE-Ovary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96278736; PubMed=8662675;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Thymus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rissuE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98010630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endocrinology 136:232-241(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aritomi M., Kunishima N., Inohara N., Ishibashi Y., Ohta S.,
                                                                                                                                                                                                                                                                                                                                                                                                                       "Crystal structure of rat Bcl-xL. Implications for the function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      œ
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                                                                                                                                                                                                                                       FUNCTION: Potent inhibitor of cell death. Inhibits activation of EUNCTION: Potent inhibitor of cell death. Inhibits activation of caspases (By similarity). Appears to regulate cell death by blocking the volatage-dependent anion channel (VDAC) by binding to it and preventing the release of the caspase activator, cytochrome c, from the mitochondrial membrane. The BC1-X(S) and BC1-X(beta) isoforms promote apoptosis.

SUBUNIT: BC1-X(L) forms heterodimers with BAX, BAK and BC1-2 (By SUBUNIT: BC1-X(L) forms heterodimers with BAX.
                                                         AND BCL-X(BETA); ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES. BCL-X(BETA) IS
SPECIFICALLY EXPRESSED IN CEREBELLUM, HEART, AND THYMUS. IN THE
OVARY, THE PREDOMINANT FORM IS BCL-X(L), WITH A SMALL BUT
                                                                                                                                                                             similarity). Heterodimerization with BAX does not seem to be required for anti-apoptotic activity (By similarity). SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
                                                                                                                                       ENVELOPE (BY SIMILARITY).

ALTERNATIVE PRODUCTS: 3 ISOFORMS; BCL-X(L) (SHOWN HERE), BCL-X(S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DEC-1994) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=9346936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hardwick J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murinae;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X82537; CAA57886.1; -. EMBL; X82537; CAA57887.1; -. EMBL; U10579; AAA19257.1; -. EMBL; U72350; AAB17353.1; -. EMBL; U72349; AAB17352.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR002475; BCL2_f
Interpro; IPR003193; BH4.
Interpro; IPR003193; BH2.
Interpro; IPR003712; Bcl_2.
Pfam; PF00452; Bcl-2; 1.
Pfam; PF02180; BH4; 1.
                                                                                                                                                                         CONFLICT
CONFLICT
CONFLICT
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SEQUENCE
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CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00337; BCL; SMART; SM00265; BH4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDB; lAF3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; S78284; AAC60702.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE: PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01260; BH4_1; 1.
PROSITE; PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                          VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                         3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                          VARSPLIC
                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      with other Bcl2 family members and for repression of cell death.

- PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity (BP similarity).

- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).

- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
 66
                        29 CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
                                                                              11 RALVADFVGYKLRQKGY-----
                                                     σ
NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124
                                                   RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEPERETPSAINGNPSWHLADSPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S76513; AAC60701.1; ALT_INIT.
                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS50062; BCL2_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mitochondrion;
                                                                                                                                                                          6
12
64
81
119
143
199
201
233 AA;
                                                                                                          Conservative
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86
129
180
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210
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233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                        42.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BCL2_family.
                                                                                                                                                                               26158 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Alternative splicing; Transmembrane;
                                                                                                           22; Mismatches
                                                                                                                                                                                                                  R -> Q (IN REF. 1
F -> S (IN REF. 2
A -> E (IN REF. 2
I -> L (IN REF. 4
A -> V (IN REF. 4
B -> SS (IN REF. 4
                                                                                                                        Score 428.5; DB Pred. No. 2e-31;
                                                                                                                                                                                          A -> T (IN REF. 4).
A -> P (IN REF. 4).
                                                                                                                                                                                                                                                                                                                             DTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
                                                                                                                                                                                                                                                                                                                                          MISSING
                                                                                                                                                                                                                                                                                                   IDYSGDIPGLL (IN ISOFORM BCL-X(BETA)).
                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                             -> P (IN REF. 4).
2B62B6C63864BC8F CRC64;
                                                                                                                                                                                                                                                                                                                 VRTTPLVCPPLVCLSSVEIPNCPFWSPGMVVED
                                                                                                                                                                                                                                                                                                                                            (IN ISOFORM BCL-X(S))
                                                                                                                                                                                                                       (IN REF.
                                                                                                                                     DB 1; Length 233;
                                                                                                                                                                                                                                    4
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                                                                                                              Indels
                                                                                                               53;
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                                                                                                              Gaps
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RESCUED BELL LINE BY L
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                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                           I- DOMAIN: The BH4 domain is required for anti-apoptotic for interaction with RAF-1 (By similarity).
If or interaction with RAF-1 (By similarity).
ISIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
ISIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
ISIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
ISIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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Eguchi Y., Ewert D.L., Tsujimoto Y.;
"Isolation and characterization of the chicken bcl-2 gene: expression
in a variety of tissues including lymphoid and neuronal organs in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          000709;
00-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cazals-Hatem D.L., Louie D.C., Tanaka S., Reed J.C.;
"Molecular cloning and DNA sequence analysis of cDNA encoding chicken homologue of the Bcl-2 oncorrotein.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92379084; PubMed=1511008;
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SEQUENCE FROM N.A.

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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apoptosis regulator Bc1-2.
BCL2 OR BCL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nomologue of the Bcl-2 oncoprotein.";
Nochim. Biophys. Acta 1132:109-113(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic Acids Res.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1 and RAF-1 (By similarity). SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum. TISSUE SPECIFICITY: In adult chicken expressed, in thymus, spleen, kidney, heart, ovary and brain, with the highest levels in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thymus. In the embryo, highly levels expressed in all tissues with high levels in the bursa of Fabricius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the caspases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (APAF-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGGWDTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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Best Local
                                                                                                                                                                   2_BOVIN
BCL2_BOVIN
002718;
                       SEQUENCE FROM N.A.
STRAIN=HOLSTEIN; TISSUE=Thymus;
                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Apoptosis regulator Bcl-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
CONFLICT
SEQUENCE
             Reyes R.A.,
                                                                  Mammalia; Eutheri
Bovidae; Bovinae;
                                                         NCBI_TaxID=9913;
                                                                                         Eukaryota;
                                                                                                   Bos taurus (Bovine).
Bovine leukemia virus associated-leukemogenesis is correlated
                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                190 DAFVELYGN----SMRPLEDESWISLKTILS-LVLVGACITLGAYLGHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D11382; BAA01978.1; -.
EMBL; D11381; BAA01978.1; JOINED.
EMBL; Z11961; CAA78018.1; -.
PIR; A37332; A37332.
PIR; S24390; S24390.
                                                                                                                                                                                                                                                  145 AEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000712; Bcl_2. Pfam; PF00452; Bcl-2; 1. Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                             130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002475; BCL2
InterPro; IPR003093; BH4.
                                                                                                                                                                                                                                                                                                                                               42
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                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                  9 DTRALVADFVGYKLRQKGYVCGAG-----PGEGPAADP------
                                                                                                                                                                                                                                                                       ELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGW 144
                                                                                                                                                                                                                                                                                                                                                            DNRETVLKYIHYKLSQRGYDWAAGEDRPPVPPAPAPAAAPAAVAAAGASSHHRPEPPGSA 69
                                                                                                                                                                                                                                                                                                                   AASEVPPAEGLRPAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTAHGRFVAVVE 129
                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q07817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS0062; BCL2_FAMILY; 1.
PS01080; BH1; 1.
PS01258; BH2; 1.
PS01259; BH3; 1.
PS01259; BH3; 1.
PS01260; BH4 1; 1.
PS01260; BH4_2; 1.
                                                                           ; Metazoa; Chordata; Crania
Eutheria; Cetartiodactyla;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR002475; BCL2_family.
             Cockerell G.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10
87
130
181
208
64
67
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139
                                                                                                                                                                                                                                                                                                                                        ------LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSD
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                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                   Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
139
                                                                                     Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              25687 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                    42.1%;
38.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                          32;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 423.5; DB 1;
Pred. No. 5.5e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G -> V (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
E -> S (IN REF. 2
GSAAASEVPPAEGLRP
                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              5252555ACB6E4C3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                           Ruminantia;
                                                                                                                                                                            229
                                                                                                                                                                           A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2).
RP -> ARLLLVRCPRLRGCA
                                                                           Pecora;
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                        49;
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with suppression of programmed cell death and increased expression
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                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00452; Bcl-2; Pfam; PF02180; BH4; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U92434; AAB53319.1; HSSP; Q07817; 1MAZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between
                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002475; BCL2_family.
                                                                               TRANSMEN
                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity (By similarity).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoletic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding t the apoptosis-activating factor (APAF-1) (By similarity). BAK an SUBPURIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and perfectly interest and services of the servic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOR interaction with RAF-1 (By similarity).

FTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle(By similarity). In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases. Dephosphorylated by protein phosphatase 2A (PP2A) (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1 and RAF-1 (By similarity). SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN: The BH4 domain is required for anti-apoptotic activity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM00337; BCL; 1
SM00265; BH4; 1
                                                                                                                                                                                                                                                                                                                                                                         PS50062;
PS01080;
PS01258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      non-profit
                                                                                                                                                                                                                                                                                                                                                     PS01259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MAR-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR000712; Bcl_2.
                                                                                                                                                                                                                                                                      Transmembrane;
     A,
                                                                                                                                                                                                                                                                                                                                                                                                                                  BCL2_FAMILY; 1.
                               30
68
72
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192
223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BH4.
                                                                                                                                                                                                                                                                      Mitochondrion; Phosphorylation
     WW;
                         POTENTIAL.

CLEAVAGE (BY CASPASES) (BY SIMILARITY)
PHOSPHORYLATION (BY PKC) (BY SIMILARITY)
                                                                                                                                                                                                                   POLY-PRO
  ADIDDOAF98FFF11D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Usage
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                         (BY SIMILARITY).
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     RESULT
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-SPRAGUE-DAWLEY; TISSUE-Ovary;

MEDLINB-95129487; PubMed-7828536;

Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;

"Expression of members of the bcl-2 gene family in the immature rat ovary: equine chorionic gonadotropin mediated inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.";

Endocrinology 136:232-241(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Brain;
MEDLINE=94193015; PubMed=8144041;
Sato T., Irie S., Krajewski S., R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P49950; 062837; Q64032;
01-0CT-1996 (Rel. 34, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 19-172 FROM N.A. MEDLINE=95059917; PubMed=7969891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";
Gene 140:291-292(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BCL2 OR BCL-2
                                          -
                                                                                                                                                                                                                                          Neuroscience 61:165-177(1994).
                                                                                                                                                                                                                                                                           "bcl-2 messenger RNA is localized adult rat brain.";
                                                                                                                                                                                                                                                                                                                    Lindholm D.;
                                                                                                                                                                                                                                                                                                                                   Castren E., Ohga Y., Berzaghi M.P., Tzimagiorgis G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apoptosis regulator Bcl-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 ALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130
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release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (APAR-1).

SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and BC1-x(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1 and RAF-1 (By similarity). SUBCELULIAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum. TISSUE SPECIFICITY: Expressed in a variety of tissues, with
                                                                                                                                                                 FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoletic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNREIVMKYIHYKLSQRGYEWDAGDAGAAPPGAAPAPGILSSQPGRTPAPSRTSPPPPPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DGVNWGRIVAFFEFGGVMCVESVNREMSPLVDSIALWMTEYLNRHLHTWIQDNGGWDAFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q62837;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD; ; Q64032;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.4%; 38.2%;
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Pred. No. 2.3e-30
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                                                                                                                                                                                                                                                                                                      of the
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STEETER STEETER STORES AND DESTRUCTION OF THE STEETER 
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Best Local
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CONFLICT
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anti-apoptotic activity Growth factor-stimulated phosphorylation
on Ser-70 by PKC is required for the anti-apoptosis activity and
occurs during the G2/M phase of the cell cycle. In the absence of
growth factors, Bcl2 appears to be phosphorylated by other protein
kinases such as ERKs and stress-activated kinases.
Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).
-i- PTM: Proteolytically cleaved by caspases during apoptosis. The
cleaved protein, lacking the BH4 domain, has pro-apoptotic
activity, causes the release of cytochrome c into the cytosol
promoting further caspase activity (By similarity).
-i- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-i- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-i- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH4).
-i- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                 SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50062; BCL2_FAMILY; PROSITE; PS01080; BH1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arPro; IPR002475; BCL2_fa

srPro; IPR003093; BH4.

srPro; IPR000712; BCL_2.

n; PF00452; BCL-2; 1.

n; PF02180; BH4; 1.
DNREIVMKYIHYKLSQRGYEWDTGDEDSAPLRAAPTPGIFSFQPESNRTPAVHRDTAART 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAF-1 (By similarity).
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                                                       DTRALVADFVGYKLRQKGY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L14680; AAA53662.1; -.
U34964; AAA77687.1; -.
S74122; -; NOT_ANNOTATE
Q07817; 1MAZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SM00337; BCL;
SM00265; BH4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E; PS01258; BH2; 1.
E; PS01259; BH3; 1.
E; PS01260; BH4_1; 1.
E; PS01063; BH4_2; 1.
                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane;
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                                                                                                            Conservative
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104
152
199
230
35
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70
42
157
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                                                                                                                                   41.18; 36.28;
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                                                                                                                                                                                                                                                        BH3.
BH1.
BH2.
CLEAVAGE (BY CASPASES) (BY SIMILARITY).
PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
A -> R (IN REF. 2).
E -> G (IN REF. 1).
S -> Y (IN REF. 2).
L -> Q (IN REF. 2).
L -> Q (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitochondrion; Phosphorylation
                                                                                                               34;
                                                                                                                                   Score 414; DB 1
Pred. No. 4e-30;
                                                                                                                                                                                                                                             E7688CB9071A872A CRC64;
                                                                                                               Mismatches
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                                                                                                                                                              <u>ب</u>
                                                                                                            62;
                                                                                                                                                            Length 236;
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RESULT
BCL2_MC
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                                                                                                                                                                                                                                                                                                Deng X., Ito T., Carr B., Mumby M., May W.S. Jr.;
"Reversible phosphorylation of Bcl2 following interl
bryostatin 1 is mediated by direct interaction with
phosphatase 2A*.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97277291; PubMed=9115213; Ito T., Deng X., Carr B., May W.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P10417; P10418;
01-MAR-1989 (Rel. 10, Created)
01-APR-1993 (Rel. 25, Last sequence up
01-MAR-2002 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99069407;
                                                                                                                                                                                                                                                                                                                                                                                       DEPHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-BALB/C; TISSUE-Liver; MEDLINE-87187643; PubMed-3032455;
                                                                                                                                                                                                                                                                                                                                                                                                                  "Bcl-2 phosphorylation required for a J. Biol. Chem. 272:11671-11673(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION BY PKC, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Res. 20:4187-4192(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in a variety of tissues including lymphoid
adult and embryo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92375724; PubMe
Eguchi Y., Ewert D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Negrini M., Silini E., Kozak C., Tsujimoto Y., Croce C.M.; "Molecular analysis of mbcl-2: structure and expression of the muringene homologous to the human gene involved in follicular lymphoma."; Cell 49:455-463(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apoptosis regulator Bcl-2 BCL2 OR BCL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BCL2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'Isolation and characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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                                           SUBUNIT: Forms homodimers, and heterodimers with BAX, Bcl-x(L). Heterodimerization with BAX requires intact domains, and is necessary for anti-apoptotic activity similarity). Also interacts with APAF-1 and RAF-1. SUBCELLULAR LOCATION: Outer mitochondrial membrane, in membrane of the nuclear envelope and the endoplasmic ralifernative products: 2 isoforms; alpha (shown here) a
 are produced by alternative splicing. TISSUE SPECIFICITY: Expressed in a va DOMAIN: The BH4 domain is required fo
                                                                                                                                                                              FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding the
                                                                                                                                                                the apoptosis-activating factor (APAF-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGWDAFVELYG - - - - PSMRPLFDFSWLSLKTLLSLAL - VGACITLGAYLGHK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPLRPLVANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129
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                                                                                                                                                                                                                                                                                    Chem.
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                                                                                                                                                                                                                                                                                    273:34157-34163(1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=1508712;
D.L., Tsujimoto Y.;
                                                                                                                                                                                                                                                                                                                                                                     PubMed=9852076;
                                                                                                                                                                                                                                                                                                                                                                                   BY PP2A
                                                                                                                                                                                                                                                                                                                                                                                                                                    required for anti-apoptosis function
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required
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following interleukin
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variety of tissues.
for anti-apoptotic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bcl-2 gene: expression
                                                here) and
                                                                                                                                                                                                                                                                                                                  protein
                                                                                 intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the murine
                                                                                                                                                                                by binding to
                                                               reticulum
                                                                                                              BAD,
BH1 (
 activity
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                                                  beta;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                             SMARY; SM00337; BGL; 1.

SMARY; SM00355; BH4; 1.

PROSITE; PS50062; BGL2_FAMILY; 1.

PROSITE; PS01080; BH1; 1.

PROSITE; PS01080; BH2; 1.

PROSITE; PS01259; BH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                         Phosphorylation.
DOMAIN
10
DOMAIN
90
DOMAIN
133
DOMAIN
184
TRANSMEM
209
SITE
34
MOD_RES
70
                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                               VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                          Apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00452; Bcl-2; Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                               MIAMOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002475; BCL2_family.
InterPro; IPR003093; BH4.
InterPro; IPR000712; Bcl_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
70 SPLRPLVATAGPALSPVPPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129
                                                                         10
                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -
                                                                                             9 DTRALVADFVGYKLRQKGYYCGAG------PG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activity, causes the release of cycochrome c into the cytos promoting further caspase activity.

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                              -----EGPAADP-----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                                                             DNREIVMKYIHYKLSQRGYEWDAGDADAAPLGAAPTPGIFSFQPESNPMPAVHREMAART 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle. In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and Stress-activated kinases. Dephosphorylated by protein phosphatase 2A (PP2A). PPM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Q07817; 1MAZ.
MGI:88138; Bcl2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B25960; TVMSB1.
E37332; E37332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A25960; TVMSA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for interaction with RAF-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L31532; AAA37282.1; -. M16506; AAA37282.1; JOINED. M16506; AAA37281.1; -.
                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      PS01260; BH4_1; 1.
PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                       Alternative
                                                                                                                                                                                                                 236 AA;
                                                                                                                                    Conservative
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104
152
199
230
230
35
70
236
                                                                                                                                              41.0%;
                                                                                                                                                                                                               26425
                                                                                                                                                                                                                                                                                                                                                                                splicing; Transmembrane; Mitochondrion;
                                                                                                                                                                                                             MW;
                                                                                                                               34; Mismatches
                                                                                                                                            Score 413; DB 1;
Pred. No. 4.9e-30;
                                                                                                                                                                                                            POTENTIAL.
CLEAVAGE (BY CASPASES) (BY SIMILARITY).
PHOSPHORYLATION (BY PKC).
DAFVELYGPSMRPLFDFSWLSLKTLLSLALVGACITLGAYL
GHK -- VGACLIVE (IN ISOFORM BETA).
                                                                                                                                                           Length 236;
                                                                                                                             Indels
                                                                                                                             52;
                                                                                                                        Gaps
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     apoptosis
          Yin X.-M., Oltvai Z.N., Korsmeyer S.J., BH1 and BH2 domains of Bcl-2 are required for inhibition of
                                                   MEDLINE=94239528;
                                                                                                                                                                                                                                     oncogenes of non-Hodgkin's lymphomas.";
                                                                                                                                                                                                                                                Tanaka S., Louie D.C., Kant J.A., Reed J.C., Frequent incidence of somatic mutations in translocated BCL2
                                                                                                                                                                                                                                                                                   MEDLINE=92096610; PubMed=1339299;
                                                                                                                                                                                                                                                                                                                                                  "Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2-1g fusion gene in lymphoma.";
                                                                                                                    "Bcl-2 is an inner mitochondrial membrane protein that blocks programmed cell death.";
                                                                                                                                                      Hockenbery D., Nunez G.,
                                                                                                                                                                   MEDLINE=91066924; PubMed=2250705;
                                                                                                                                                                                      SUBCELLULAR LOCATION.
                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-131 FROM N.A. (ISOFORM ALPHA), AND VARIANTS NHL
                                                                                                                                                                                                                                                                                                                                                                                           Seto M., Jaeger U., Hockett R.D., Graninger W., Bennett S., Goldman P., Korsmeyer S.J.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cleary M.L., Smith S.D., Sklar J.; "Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglobul transcript resulting from the t(14;18)
                                                                                                                                                                                                                                                                                                                                         EMBO J. 7:123-131(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=88196071; PubMed=2834197;
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM ALPHA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translocation.";
Cell 47:19-28(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM ALPHA MEDLINE=87002488; PubMed=2875799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=923/5/24; runcu Elegation of Y.; Eguchi Y., Ewert D.L., Tsujimoto Y.; Eguchi Y., Ewert D.L., Tsujimoto Y.; "Isolation and characterization of the chicken bcl-2 gene: expression "Isolation and retreamed including lymphoid and neuronal organs in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCL2_HUMAN STANDARD; PRT; 239 AA
P10415; P10416; Q15197; Q13842;
Q1-MAR-1989 (Rel. 10, Created)
Q1-APR-1993 (Rel. 25, Last sequence update)
Q1-MAR-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 20:4187-4192(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVISIONS TO 96; 110 AND 237.
MEDLINE=92375724; PubMed=1508712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tsujimoto Y., Croce C.M.;
"Analysis of the structure, transcripts, and protein products
"Analysis of the involved in human follicular lymphoma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA) MEDLINE=86259760; PubMed=3523487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apoptosis regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 GGWDAFVELYG----PSMRPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
                                                                                                                                                                                                                      79:229-237(1992).
                                                                                                  mmed cell death.";
348:334-336(1990).
     and
heterodimerization with Bax.";
                                                  PubMed=8183370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ISOFORM ALPHA).
                                                                                                                                                    Milliman C.
                                                                                                                                             Schreiber R.D., Korsmeyer S.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 AA
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"BCL-2 is phosphorylated and inactivated by an ASK1/Jun N-terminal protein kinase pathway normally activated at G(2)/M."; Mol. Cell. Biol. 19:8469-8478/1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 278:1966-1988(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98057466; PubMed-9395403;
Cheng E.H.-Y., Kirsch D.G., Clem R.J., Ravi R., Kastan M.B., Bedi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLEAVAGE BY CASPASES,
                                                                                                                                                                                                                                                                                                                                                                                                                    anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle. In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases. behosphorylated by protein phosphatase 2A (PP2A) (By similarity). Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity.

DISEASE: Involved in follicular lymphoma (FL) (also known as type II chronic lymphatic leukemia) by a chromosomal translocation ti(14;18)(q32;q21) which involves Bcl2 and immunoglobulin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ruvolo P.P., Deng X., May W.S.;
"Phosphorylation of Bc12 and regulation of apoptosis.";
Leukemia 15:515-522(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ueno K., Hardwick J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 369:321-323(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21260650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Conversion of Bcl-2 to a Bax-like death effector by caspases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20036804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVIEW ON PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION BY ASK1/JNK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                      EMBL;
                                                               EMBL;
                                                                                 EMBL; M13994;
                                                                                                                            or send an
                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                  use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1 and RAF-1. SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum. ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta; ALTERNATIVE PRODUCTS: 1soforms; alpha (shown here)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells.
                                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    are produced by alternative splicing.
TISSUE SPECIFICITY: Expressed in a variety of tissues.
DOMAIN: The BH4 domain is required for anti-apoptotic activity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             release of cytochrome c from the mitochondria and/or by binding to the apoptosis activating factor (APAF-1).
M13995;
M14745;
X06487;
S72602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interaction with RAF-1.
                                                                                                                            email to license@isb-sib.ch).
                      AAA51814.1; ALT_SEQ
AAA35591.1; ...
CAA29778.1; -.
                                                                                     AAA51813.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=10567572;
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      ALT_SEQ
                                                                                                                                                                                  and for
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Best Local S
Matches 87
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InterPro; IPR000712; Bc
Pfam; PF00452; Bc1-2; 1
Pfam; PF02180; BH4; 1
SMART; SM00337; BCL; 1
SMART; SM00265; BH4; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
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                                                                                                                                                                                                                                          CONFLICT
CONFLICT
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SEQUENCE
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MIM; 151430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proto-oncogene; Apoptosis; Alternative splicing; Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                              VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT
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190 QDNGGWDAFVELYG----PSMRPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK
                      139 HSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                    79
                                                                                                                  36
                                                                                                                                       10 DNREIVMKYIHYKLSQRGYEWDAGDVGAAPPGAAPAPGIFSSQPGHTPHPAASRDPVART 69
                                                                                          70 SPLQTPAAPGAAAGPALSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARGR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; B29409; TVHUB1.
; A24428; TVHUBC.
; C37332; C37332.
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B29409; TVHUB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q07817; 1MAZ
                                                                                                                                                               DTRALVADFVGYKLRQKGYVCGAG------
                                              FATVVEELFRDGVNWGRIVAFFEEGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWI
                                                                   FTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWI 138
                                                                                                                                                                                     1 Similarity
87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS01259; BH3; 1.
PS01260; BH4_1; 1.
PS50063; BH4_2; 1.
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PS01080; BH1; 1.
PS01258; BH2; 1.
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                                                                                                                                                                                                                                              239 AA;
                                                                                                                                                                                                                                                                                                                                      34
64
145
                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  59
                                                                                                                                                                                                                                                                                                                                                                                                 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disease mutation
                                                                                                                 ----GPAADP----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQR 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphorylation; Chromosomal translocation;
                                                                                                                                                                                                                                                         48
59
117
129
                                                                                                                                                                                                                                                                                                                 188
                                                                                                                                                                                                                                                                                                                                                                                                 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bc1_2.
                                                                                                                                                                                                  41.0%;
                                                                                                                                                                                                                                               26266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BCL2_family.
                                                                                                                                                                                                                                                WW.
                                                                                                                                                                                        34; Mismatches
                                                                                                                                                                                                                                                         LOSS OF ANTI-APOPTOTIC ACTIVITY.

1 -> F (IN REF. 4).

P -> T (IN REF. 3).

S -> R (IN REF. 3).

R -> C (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DAFVELYGPSMRPLFDFSWLSLKTLLSLALVGACITLGAYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION (BY PKC) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLEAVAGE (BY CASPASE-3)
                                                                                                                                                                                                    Pred.
                                                                                                                                                                                                                                                                                                                 LOSS OF ANTI-APOPTOTIC ACTIVITY. W->A: NO HETERODIMERIZATION WITH BAX AND
                                                                                                                                                                                                    Score 412.5;
Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                                                                      MUTATION)
                                                                                                                                                                                                                                                                                                                                                                                                                                              /FTId=VAR_000827
                                                                                                                                                                                                                                                                                                                                                                          /FTId=VAR_000829
                                                                                                                                                                                                                                               3C49F2B714DC9CCB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 I (IN NON-HODGKINS-LYMPHOMA; SOMATIC
                                                                                                                                                                                                                                                                                                                                                                                                                                 S (IN NON-HODGKINS-LYMPHOMA; SOMATIC
                                                                                                                                                                                                                                                                                                                                                    ABOLISHES CLEAVAGE BY CASPASE-3
NO EFFECT ON CLEAVAGE BY CASPASI
                                                                                                                                                                                                                                                                                                                                          NO HETERODIMERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGASGDVS (IN ISOFORM BETA)
                                                                                                                                                                   -----PGE-----
                                                                                                                                                                                                      .5e-30;
                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                               Length 239;
                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                            WITH BAX AND
                                                                                                                                                                                                                                                                                                                                                      BY CASPASE-3
                                                                                                                                                                                            55;
                                                                                                                                                                                            Gaps
                                                                                                                                                                                             <u>ن</u>
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BCL2_CRILO
Q9JJV8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRILO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apoptosis regulator Bcl-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tomicic M.T., Christmann M., Kaina B.;
"Cloning and functional analysis of cDNA encoding the hamster Bcl-2
profein ":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20431763; PubMed=10973819;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Ovary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                   cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytos promoting further caspase activity.

Promoting further caspase activity.

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND CLEAVAGE E MEDLINE=21092839; PubMed=11181062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tomicic M.T., Kaina B.: "Hamster Bc1-2 protein is cleaved in vitro and in cells by caspase-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem. Biophys. Res. Commun. 275:899-903(2000).
                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum. DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAF-1 (By similarity).

PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 prM: Phosphorylation/dephosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle (By similarity). In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERXs and stress-activated kinases by other protein kinases such as ERXs and stress-activated kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding the apoptosis-activating factor (APAF-1) (By similarity). BAK arguments becomes activating factor (APAF-1) and the system of the poptosis activating factor (APAF-1) and the poptosis activation and the poptosis activat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bhem. Biophys. Res. Commun. 281:404-408(2001).
FUNCTION: Suppresses apoptosis in a variety of cell systems
including factor-dependent lymphohematopoietic and neural cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1 and RAF-1 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTM: Proteolytically cleaved by caspases during apoptosis. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (By similarity). Dephosphorylated by protein phosphatase
   AJ271720; CAB92245.1; -. P53563; 1AF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND CLEAVAGE BY CASPASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaina B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 AA
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 AR11_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                             AR11_XENLA
Q91828;
Q1-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00452; Bc1-2;
Pfam; PF02180; BH4; 1.
SMART; SM00337; BCL; 1
SMART; SM00265; BH4; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50062; PROSITE; PS01080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002475;
InterPro; IPR003093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
Apoptosis regulator R11 (xR11).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
Cell-Survival genes.";
Gene 158:171-179(1955).
Gene 158:171-179(1955).
-!- FUNCTION: CONFERS STRONG PROTECTION AGAINST CELL DEATH.
-!- SUBCELLULAR LOCARION: Membrane-bound (Potential).
-!- SUBCELLULAR STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN BRAIN OF MID-METAMORPHOSIC TO POST-METAMORPHOSIC TADPOLES AND BRAIN OF MID-METAMORPHOSIC TO POST-METAMORPHOSIC TADPOLES AND ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.
-!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                      Xenopus laevis (African clawed frog)
                                                                                                                                          Cruz-Reyes J., Tata J.R.;
                                                                                                                                                           MEDLINE=95331613; PubMed=7607538;
                                                                                                                                                                                                                 NCBI_TaxID=8355;
                                                                                                                                                                                                                              Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN 189
                                                                                                                              "Cloning,
                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                               190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 DNREIVMKYIHYKLSQRGYEWDVGDVDAAPLGAAPTPGIFSFQPESNPTPAVHRDMAART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 -----VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 DTRALVADFVGYKLRQKGY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPLRPIVATTGPTLSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129
                                                                                                                                                                                                                                                                                                                                                                                                                               GGWDAFVELYG----PSVRPLFDFSWLSLKTLLSLAL-VGACITLGTYLGHK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS50063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS01259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR000712; Bcl_2.
                                                                                                                             characterization and expression of two Xenopus bcl-2-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                             (Rel. 35, Created)
                                                                                                                                                                                                                                Xenopus.
                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BH4_1; 1.
BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            вн3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BCL2_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26491 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         вн4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BCL2_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitochondrion; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 403; DB 1;
Pred. No. 3.8e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           вн2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLEAVAGE (BY CASPASE-3 AND CASPASE-9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BECADF1EF3337228 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                204
                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Search completed: June 10, 2002, 10:32:13 Job time: 346 sec
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                                                                                                                                                                                                                                                                                                              Дβ
                                                                                                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 36.8%; Score 371; DB 1; Length 204; Best Local Similarity 42.1%; Pred. No. 2.4e-26; Matches 82; Conservative 25; Mismatches 62; Indels 26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPRO02475; BCL2_family.
InterPro; IPRO03093; BH4_
InterPro; IPRO0712; BCL2.
Pfam; PF00452; BCl-2; 1_
Pfam; PF02480; BH4; 1.
SMART; SM00337; BCL; 1.
SMART; SM00235; BH4; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01080; BH2; 1.
PROSITE; PS01080; BCL2_FAMILY; 1.
APOPCOSIS; Transmembrane.
Bu1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X82461; CAA57844.1; -. HSSP; Q07817; IMAZ.
                                                                                     184 RLLTI-VMLTGVFAL 197
                                                                                                                        166 NWASVRTVLTGAVAL 180
                                                                                                                                                     124 VESANKEMTDLLPRIVQWMVNYLEHTLQPWMQENGGWEAFVGLYGKNAAAQSRESQERFG 183
                                                                                                                                                                              108 AESVNKEMEPLVGQVQEWNVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLRE--G 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                           64 EATEEFELRYQRAFSDLTSQLHITQDTAQQSFQQVMGELFRDGTNWGRIVAFFSFGRALC 123
                                                                                                                                                                                                                                                                                                                                     48 AAGDEFETRERRIFSDLAAQLHVIPGSAQQRETQVSDELFQGGPNWGRLVAFFVFGAALC 107
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                                                                                                                                                                                                                                                                                                  SRDLVEKFVSKKLSQ-NEACRKFSNNPNPMPYLMEPSTSERPGEGATQGIVEEEVLQALL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 120 BH1.
152 167 BH2.
181 198 POTENTIAL,
204 AA; 23379 MW; 3BFC6BE6DDA4CA03 CRC64;
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Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                   Database
                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Run on:
SPTREMBL_19:*

SP_REMBL_19:*

Sp_archea:*

Sp_bacteria

Sp_fungl:*

Sp_human:*

Sp_invert

Sp_invert

Sp_mamma

Sp_mamma

Sp_mamma

Sp_mamma

Sp_pha

10:
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SF

17:
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                                                                                                                                                                                                                                                                                                                                                                         seq length: 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                      562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapop 10.0 ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MATPASAPDTRALVADFVGY.....LTGAVALGALVTVGAFFASK 193
 sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                           sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                  sp_archea:*
sp_bacteria:*
                                                                                                                                                                                        sp_invertebrate:*
                                                                             sp_rodent:*
                                                                                                                                                                     sp_mammal:*
                                                                                                           sp_plant:*
                                                                sp_vertebrate:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

16	15	14	13	12	11	10	9	8	7	6	ر ن	4	ω	2	<b>_</b>	Result No.
347	373	373.5	374.5	374.5	398.5	399	401	401	403	428.5	431.5	435.5	440.5	761	996	Score
34.5	37.0	37.1	37.2	37.2	39.6	39.6	39.8	39.8	40.0	42.6	42.9	43.2	43.7	75.6	98.9	Query Match I
219	204	188	235	188	180	236	217	180	238	233	233	233	233	178	193	Query Match Length DB
11	13	4	11	11	σ	11	11	6	13	σ	0	11	0	11	11	: BB
Q99N36	Q90ZH2	Q9H1R6	035843	Q9QWX2	Q9BDX7	Q923R6	Q99N35	Q9BDD5	Q90Z98	Q9MZS7	Q9N1A2	035844	Q9MYW4	Q9CYW5	088996	ID
Q99n36 mus musculu	Q90zh2 xenopus lae	Q9h1r6 homo sapien	O35843 mus musculu	Q9qwx2 mus musculu	Q9bdx7 bos taurus	Q923r6 cricetulus	Q99n35 mus musculu	Q9bdd5 bos taurus	Q90z98 brachydanio	Q9mzs7 ovis aries	Q9n1a2 sus scrofa	O35844 mus musculu	Q9myw4 oryctolagus	Q9cyw5 mus musculu	O88996 rattus norv	Description

Query Match

98.98;

Score 996;

DB 11;

Length 193;

44	43	42	41	40	39	38	37	36	ω 5	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
121.5 117	122.5	123.5	125	125.5	130.5	130.5	130.5	131	131.5	135	135	139	141	142.5	143	144	146.5	148.5	153	159.5	162	163	168.5	171.5	176.5	185	189
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204	91	331	174	330	213	213	213	162	213	212	114	211	255	179	177	149	179	218	173	163	235	58	125	221	192	170	209
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Q923W6 Q9HD36	Q923W5	P97287	Q9W6F2	Q9Z1P3	Q9DGJ5	Q91812	Q9UL32	Q9DH00	035425	Q9UMX3	Q9NR76	Q9W6F1	Q919N3	Q9E1F2	Q90ZN1	Q9GMG7	Q9NYG7	Q9N754	Q9JKL3	Q9MZS6	Q967D2	Q9R1B3	Q9H1R5	Q98U13	Q919N4	Q9WUI5	Q9JK59
Q923w6 peromyscus Q9hd36 homo sapien		mus mu	Q9w6f2 gallus gall	rattus		Q9i8i2 gallus gall	Q9ul32 homo sapien	Q9dh00 meleagrid h	035425 rattus norv	Q9umx3 homo sapien	Q9nr76 homo sapien	Q9w6f1 gallus gall			Q90zn1 gallus gall	0	Q9nyg7 homo sapien	Q9n754 suberites d	Q9jkl3 rattus norv	Q9mzs6 ovis aries	Q967d2 geodia cydo	ω	⋾	Q98u13 xenopus lae	Q9i9n4 brachydanio	Q9wui5 rattus norv	Q9jk59 rattus norv

## ALIGNMENTS

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008996
ACC 00C EE EG OCC OCC EE EG O
                                           Interpro; | IPRO02475; BCL2_family. |
Interpro; | IPRO00712; Bcl_2. |
Interpro; | IPRO000712; Bcl_2. |
Interpro; | IPRO03093; Bbl4. |
Pfam; | PF00452; Bcl_2; 1. |
Pfam; | PF00452; Bcl_2; 1. |
SMART; | SM00337; BcL; 1. |
SMART; | SM00337; BcL; 1. |
SMART; | SM00355; Bbl4; 1. |
PROSITE; | PS50062; Bcl2_FAMILY; 1. |
PROSITE; | PS01260; Bbl4; 1. |
PROSITE; | PS01260; Bbl4_1; 1. |
PROSITE; | PS01260; Bbl4_1; 1. |
PROSITE; | PS01260; Bbl4_1; 1. |
PROSITE; | PS01260; Bbl4_2; 1. |
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01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Differential expression of bcl-w and bcl-x messenger RNA in the developing and adult rat nervous system.";
Neuroscience 91:673-684(1999).
EMBL; AF096291; AAC64200.1; -.
HSSP; Q07817; 1MAZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN; MEDLINE-99292146; PubMed=10366024; Hamner S., Skoglosa Y., Lindholm D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BCL-W
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      193 AA;
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      20820 MW;
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            36D6742F4529AFB4 CRC64;
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Best Local Similarity

98.4%;

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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Psoole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                  PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9CYW5;
Q1-JUN-2001 (TrEMBLrel. 17,
Q1-JUN-2001 (TrEMBLrel. 17,
Q1-DEC-2001 (TrEMBLrel. 19,
BCL2-LIKE 2.
                                                                             Pfam; PF00452; Bc1-2; 1.
Pfam; PF02180; BH4; 1.
SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
                                                                                                                                                          InterPro; IPR002475; BCL2_family.
InterPro; IPR000712; Bcl_2.
InterPro; IPR003093; BH4.
                                                                                                                                                                                                                                                                   EMBL; AK013244;
                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=EMBRYO; MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
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                                                                                                                                                                                                                           MGI:108052; Bc1212.
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PS50062; BCL2_FAMILY;
PS01080; BH1; 1.
PS50063; BH4_2; 1.
178 AA; 19147 MW;
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1; Mismatches 2;
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    E2D4C3F79528E9D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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Best Local :
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PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUL-2000) to the EMBL; AY005131; AAF88137.1; HSSP; P53563; 1AF3.
                                                                                                                                                                                                                                                              PROSITE; PS50062; BCL2_FAMILY; PROSITE; PS01080; BH1; 1. PROSITE; PS01258; BH2; 1.
                                                                                                                                                                                                                                                                                                                  InterPro; IPR000712; E
InterPro; IPR003093; E
Pfam; PF00452; Bc1-2;
Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                  SMART;
                                                                                                                                                                                                                                                                                                         SMART;
                                                                                                                                                                                                                                                                                                                                                                                                      "Rabbit Bcl-X."
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9MYW4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9MYW4
                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9986
                                        126
                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002475;
                    142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 QVQEWMVAYLETRLADWIHSSGGWAEFTAL
                                                            82
                                                                                  66
                                                                                                       40
                                                                                                                                               11 RALVADFVGYKLRQKGYVC------GAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                           σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                       D-----
GGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
                  GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                        VVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMEVLVSRIAAWMATYLNDHLEPWIQEN
                                                   VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
                                                                                 NGATGHSSSLDAREVIPMTAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ
                                                                                                                           RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTGPEMETPSAINGNPAWHPADSPAV 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVQDWMVAYLETRLADWIHSSGGWVRSSQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143;
                                                                                                                                                                                                                                                                                               SM00337; BCL;
SM00265; BH4;
                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                   PS01260;
PS50063;
                                                                                                                                                                                                                                                       PS01259;
                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               Robertson L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                      вн2;
вн3;
                                                                                                      -----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                                                                                                                                                                               43.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lagomorpha;
                                                                                                                                                                                                                         25986 MW;
                                                                                                                                                                                                                                                                                                                                        вн4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.6%;
95.3%;
                                                                                                                                                                                                                                                                                                                                                            BCL2_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18,
                                                                                                                                                                                                                                                                                                                                                                                                                James
                                                                                                                                                                    22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last
                                                                                                                                                                              Score 440.5;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 761;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                         12F0F30344D53F93 CRC64;
                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                E.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leporidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150
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                                                                                                                                                                               .5e-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11;
.2e-59;
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                                                                                                                                                                                           DB
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                                                                                                                                                -----PGEGPAA. 39
                                                                                                                                                                                        Length 233;
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                                                                                                                                                                     Indels
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                                                                                                                                                                    51;
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                                                                                                                                                                   Gaps
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                                                                                  125
                                         185
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE-98051053; PubMed-9390687; Yang X.-F., Weber G.F., Cantor H.; "A novel Bcl-x isoform connected to apoptosis in T cells."; Immunity 7:629-639(1997).
EMBL; U51278; AAC53459 1; -.
HSSP; P53563; 1AF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00452; Bcl-2; 1.
Pfam; PF02180; BH4; 1.
SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
PR0SITE; PS50062; BCL2_FAMILY; 1
PR0SITE; PS01080; BH1; 1.
PR0SITE; PS01258; BH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      035844;
035844;
01-JAN-1998
01-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
PROSITE;
PROSITE;
SEQUENCE
                                            Q9NIA2 PRELIMINARY; PRT; 233 AA.
Q9NIA2;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updata
ANTI-APOPTOTIC REGULATOR BCL-XL.
  Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 01-DEC-2001 (TrEMBLrel.
                      Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BCL2L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                   141
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                                                                                                                                                                                                                   QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS 140
                                                                                                                                                                                                                                                                                                                       RALVADFVGYKLRQKGY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGI:88139; Bc121
                                                                                                                                                                                   SGGWAEFTALYGDGALEEARRLREG--NWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                     NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE
                                                                                                                                                                                                                                                                          CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT
                                                                                                                                                            NGGWDTFVDLYGNNAAAESRKGKEGFNRWFLTGMTVAGVVLLGSL
                                                                                                                                                                                                         QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE
                                                                                                                                                                                                                                                                                                  RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV
                                                                                                                                                                                                                                                                                                                                                                                           E; PS01259; BH3; 1.
E; PS01260; BH4_1; 1.
E; PS01260; BH4_2; 1.
PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                             94;
                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR002475; BCL2_family.
IPR000712; Bcl_2.
IPR003093; BH4.
  ; Metazoa;
Eutheria;
                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=THYMUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
Rodentia;
Chordata; Craniata; Vertebrata; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                       43.2%;
41.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05,
19,
                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                       Score 435.5;
Pred. No. 9.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                    3083F2D8327E072E CRC64;
                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                        update)
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                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                              229
  Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                   233;
                                                                                                                                                                                                                                                                                                                                             53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus.
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Best Local
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PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                 Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Peo
Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
[1]
                                                                                                                                                                                                                                                     O9MZS7 PRELIMINARY; PRT; 233 AA.

O9MZS7;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                         Murray J.F., Dong Y.B., Leigh A.J., "BC1-x in the sheep ovary."; submitted (JUL-1999) to the EMBL/Ger EMBL; AF164517; AAF89532.1; -. HSSP; P53563; 1AF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (DEC-1999) to the EMBL/GenBank/DDBJ EMBL; AF216205; AAF33212.1; -. HSSP; Q07817; 1MAZ.
 Pfam; PF00452; Bcl-2; 1
Pfam; PF02180; BH4; 1.
SMART; SM00337; BCL; 1
                                  InterPro; IPR002475; BCL2_family
InterPro; IPR000712; Bcl_2.
InterPro; IPR003093; BH4.
                                                                                                                                       TISSUE=OVARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00452; Bc1-2; 1
Pfam; PF02180; BH4; 1.
SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-HEART;
                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          BCL-X LONG PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002475; BCL2_family.
InterPro; IPR000712; Bcl_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "PCR Cloning of a Porcine bcl-xL cDNA from Heart.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lee T.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9823;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          σ
                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                      NGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTLAGVVLLGSL
                                                                                                                                                                                                                                                                                                                                                                                  SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL
                                                                                                                                                                                                                                                                                                                                                                                                                     QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAXLETRLADWIHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RELVVDFLSYKLSQKGYSWSQFTDVEENRTEAPEGTESEAETPSAINGNPSWHLADSPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; PS50062; BCL2_FAMILY;

3; PS01080; BH1; 1.

3; PS01258; BH2; 1.

4; PS01259; BH3; 1.

5; PS01259; BH4_1; 1.

6; PS50063; BH4_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 42.9%; Score 431.5; DB 6;
Similarity 41.8%; Pred. No. 2.2e-30;
94; Conservative 21; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR003093; BH4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26047 MW;
                                                                                                   EMBL/GenBank/DDBJ
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                                                                                                                           Scaramuzzi R.J.,
                                                                                                                                                                                                      Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                       update)
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                                                                                                     databases
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                                                                                                                                                                                                                                                                                                                                                                                               183
                                                                                                                                                                                                                   Euteleostomi;
                                                                                                                             Carter
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01-DEC-2001
01-DEC-2001
01-DEC-2001
01-DEC-2001
BCL-XL-LIKE
BLP1
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PROSITE;
PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brachydanio rerio (2ebrafish) (2ebra dar
Eukarydna; Metazoa; Chordata; Craniata;
Actinopterygii, Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                              zebrafish, Danio rerio(1).";
Biochim. Biophys. Acta 1519:127-133(2001).
EMBL; AF317837; AAK81706.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=21299061; PubMed=11406282;
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                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen M.-C.,
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  139
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                                                                                                                                                                                                                                           11 RALVADFVGYKLRQKGYVC-----
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                                                                                                                                                                                                                                                                                                          Match
rocal Similarity
                                                                                                                                                                                                                  6
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HSSGGWAEFTALYGDGALEEARRLREG - - NWA - SVRTVLTGAVALGALVTVGAFFASK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGWAEFTALYGDGALEEARRIRE--GNWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQEN 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS
                                           FESVMDEVFRDGVNWGRIVGLFAFGGALCVECVEKEMSPLVGRIAEWMTVYLDNHIQPWI
                                                                   FTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWI 138
                                                                                                                            GTPPQSPASSPQRQTNGSGGLDAVKEALRDSANEFELRYSRAFNDLSSQLHITPATAYQS
                                                                                                                                                                       --PGEGPAADPLHQ----
                                                                                                                                                                                                                  RELVVFFIKYKLSQRNYPCNHIGLTEDTNRTDGAEENGEGAAGATTLVNGTMNRTNASST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
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TTE; PS00062; BCL2_FAMILY;
TTE; PS01080; BH1; 1.
TTE; PS01258; BH2; 1.
TTE; PS01259; BH3; 1.
TTE; PS01260; BH4_1; 1.
TTE; PS01260; BH4_2; 1.
SNCE 233 AA; 26134 MW;
                                                                                                                                                                                                                                                                                                        87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C., Gong H.-Y., Cheng C., Wang J.-P., Hong
and characterization of zfBLP1, a Bcl-XL
                                                                                                                                                                                                                                                                                                                                                                                                                   238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last seq
(TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                   26253 MW;
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36.6%;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 428.5; DB Pred. No. 4e-30;
                                                                                                                                                                                                                                                                                                                        Score 403;
Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                   6E58394933EEFDDB
                                                                                                                                                     012BFA1382762915
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ata; Vertebrata; E
tei; Euteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238
                                                                                                                                                                                                                                                                                                    DB 13;
7.3e-28;
hes 62;
                                                                                                                                                                                                                                                      -GAG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hong
                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64;
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                                                                                                                                                                                                                                                                                                                                            Length
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homologue
                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                        62;
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10 PMDD5
10 PMDD7
10 PMD7
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Best Local S
Matches 76
STRAIN-129/SVJ;
Yang X.-F., Cant
"Novel cDNA stru
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NON_TER
SEQUENCE
                                                                                                                                                                                                                      01-JUN-2001 (Tremblrel. 17, 01-JUN-2001 (Tremblrel. 17, 01-DEC-2001 (Tremblrel. 19, 01-DEC-2001) (Tremblrel. 19, 01-DEC-2001) (Tremblrel. 19, 01-DEC-2001)
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ANTI-APOPTOTIC REGULATOR BCL-XL (FRAGMENT).
                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                               Q99N35;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-2000) to the EMBL; AF245488; AAK31307.1; EMBL; AF245489; AAK31308.1; HSSP; Q07817; 1MAZ.
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InterPro; IPR000712; Bcl_2.
Pfam; PF00452; Bcl_2; 1.
SMART; SM00337; BCL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bovidae; Bovinae; Bos. NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                           Q99N35
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                                                               SEQUENCE FROM N.A.
                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AALCAESVNKEMEPLVGQVQEWNVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESRKGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ERFNRWFLTGMTVAGVVLLGSL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E--GNWASVRTVLTGAVALGAL
  cDNA structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M., Bouzat J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 53.9 76; Conservative
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PS01080; BH1; 1.
PS01258; BH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS01259;
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180 AA;
                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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  and
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genomic
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                                                                                                                                                                                                                             (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183
                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rine bcl-xL gene and related EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 401; DB 6; Pred. No. 7.7e-28 9; Mismatches 4
                                                                                                                                 Craniata; Veri
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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  organization
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                                                                                                                                      Vertebrata; |
thi; Muridae;
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  of
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  apoptosis
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                                                                                                                                                           Euteleostomi;
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                                                                                                                                        Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -VVVGGLIAQK
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  regulatory
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RESULT 0933R6 AC 095 AC
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Best Local S
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                          Matches
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PROSITE; PS50062; BCL2_FAMILY; 1.

PROSITE; PS01080; BH1; 1.

PROSITE; PS01258; BH2; 1.

PROSITE; PS01259; BH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene Bcl-x-gamma.";
submitted (MAR-1999) to the EMBL/GenBank/DDBJ
EMBL; AF133282; AAK15455.1; -.
EMBL; AF133281; AAK15455.1; JOINED.
HSSP; P53563; 1AF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q923R6;
01-DEC-2001
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q923R6
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InterPro; IPR000712; Bcl_2.
Pfam; PF00452; Bcl-2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lai D.Z., Chen W., Wang H.T.; "Construction of a robust CHO cell line for biopharmaceutical use. Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF404339; AAK92201.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BCL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metázoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B-CELL LYMPHOMA PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 E--GNWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 AALCAESVNKEMEPLVGQVQEWNVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLR 163
  130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 QAMRAAGDEFETRERRTESDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 QALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFFSFG
                                                   82
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                                                                                                                                                                                                                DNREIVMKYIHYKLSQRGYEWDVGDVDAAPLGAAPTPGIFSFQPESNPTPAVHRDMAART
                                                                                                                                                                                                                                                                    DTRALVADFVGYKLRQKGY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ERFNRWFLTGMTVAGVVLLGSL 213
VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN
                                                VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHSS 141
                                                                                                         SPLRPIVATTGPTLSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT
                                                                                                                                                             ----VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ
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76; Conserv
                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217 AA; 24234 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.8%; ilarity 53.5%; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              92201.1; -.
26500 MW; BEDF052EF32CA8B8
                                                                                                                                                                                                                                                                                                                                                       39.6%;
35.3%;
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                                                                                                                                                                                                                                                                                                                             32;
                                                                                                                                                                                                                                                                                                                          Score 399; DB 11;
Pred. No. 1.6e-27;
32; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 401; DB 11;
Pred. No. 9.7e-28;
9; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3B5A4E809A7DEF18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236
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                                                                                                                                                                                                                                                                                                                                66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 217;
                                                                                                                                                                                                                                                                                                                                                                                 Length 236;
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                                                                                                                                                                                                                                                                                                                                Indels
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  189
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RESULT
Q9BDX7
  ACCOMENS TO THE PROPERTY OF TH
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Best Local :
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases EMBL; AF245487; AAK31306.1; -. HSSP; Q07817; IMAZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. Amills M., Bouzat J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ANTI-APOPTOTIC REGULATOR BCL-XL (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9BDX7
SEQUENCE FROM N.A.
MEDLINE-20350651; PubMed=10894153;
Rucker E.B. III, Dierisseau P., Wagner K.U., Garrett L.,
Wynshaw-Boris A., Flaws J.A., Hennighausen L.;
"Bcl-x and Bax regulate mouse primordial germ cell survi
                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9QWX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002475; BCL2_family
InterPro; IPR000712; Bcl_2.
Pfam; PF00452; Bcl_2; 1.
SMART; SM00337; BCL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovidae; Bovinae;
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Cetartiodactyla, Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9BDX7
                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                 BCL-X (FRAGMENT).
                                                                                                                                                                                                                                                                                                                             01-MAY-2000
01-DEC-2001
                                                                                                                                                                 NCBI_TaxID=10090
                                                                                                                                                                                                                                              Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Characterization of the bovine bcl-xL gene and related pseudogenes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190 GGWDAFVELYG----PSVRPLFDFSWLSLXTLLNLAL-VGACITLGTYLGHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 YKLROKGYYCGAGPGEGPAAD------PLHQAMRAAGDEFETRFRRTFSDLAAQLHYT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGSAQORFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLE 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DHLEPWIQENGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRLADWIHSSGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WHLEDSPAVNGA-PGHSRSSDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHIT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGTAYQSFEQVVNELFRDGVNWGRIVASFSFGGALCVESVDKEMQVLVSRIATWMATYLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS50062; BCL2_FAMILY; PS01258; BH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS01259; BH3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180
180 AA;
                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 13, (TrEMBLrel. 13, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.6%;
47.1%;
                                                                                                                                                                                              Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23;
                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 398.5; DB 6
Pred. No. 1.3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62C4C0BD0555A9EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                               188
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           cell survival
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RESULT
O35841
ID 843
ID 843
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50062; BCL2_FAMILY; 1
PROSITE; PS01080; BH1; 1
PROSITE; PS01259; BH3; 1.
PROSITE; PS01260; BH4_1; 1.
PROSITE; PS0063; BH4_2; 1.
NON_TER 188 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O35843;
O35843;
O1-JAN-1998
O1-JAN-1998
O1-DEC-2001
                                                                                                                                                                                                                       Waddine=98051053; PubMed=9390687; Yang X.-F., Weber G.F., Cantor H.
"A novel Bcl-x isoform connected apoptosis in T cells."; Immunity 7:629-639(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                               Pfam; PF00452; Pfam; PF02180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM
PROSITE;
PROSITE;
                                                                                                                 InterPro;
                                                                                                                                                                                 EMBL; U51277; AAC53458.1; -. HSSP; P53563; 1AF3.
                                                                                                                                                                                                                                                                                                                                                STRAIN=B6/CBA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BCL2L.
                                                                                            InterPro;
                                                                                                                                         InterPro;
                                                                                                                                                            MGD; MGI:88139; Bcl21.
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BCL-X-GAMMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00452; Bc1-2; 1.
Pfam; PF02180; BH4; 1.
SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002475; BCL2_family.
InterPro; IPR000712; Bcl_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P53563; 1AF3.
MGD; MGI:88139; Bc121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      apoptosis during embryogenesis.";
Mol. Endocrinol. 14:1038-1052(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003093; BH4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQEWMVAYLETRLADWIHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGGW 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE
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  SM00337;
SM00265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                       IPR002475; BCL2_family.
IPR000712; Bcl_2.
IPR003093; BH4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 05, Created)
(TrEMBLrel. 05, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                             Bc1-2; 1.
BH4; 1.
                                                                                                                                                                                                                                                                                                                                              TISSUE=THYMUS
  BCL;
BH4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21126 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.2%; Score 374.5;
42.9%; Pred. No. 1.80
tive 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4E62F8356D248E52 CRC64;
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hes 38;
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Q9H1R6
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Best Local S
Matches 79
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Best Local
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                                                                                                                                                                               InterPro; IPR002475; BCL2_family.
InterPro; IPR000712; Bcl_2.
InterPro; IPR003093; BH4.
Pfam; PF00452; Bcl_2; 1.
Pfam; PF02180; BH4; 1.
SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
PROSITE; PS50063; BH4; 1.
PROSITE; PS50063; BH4; 1.
PROSITE; PS50063; BH1; 1.
PROSITE; PS50063; BH4; 2; 1.
PROSITE; PS50063; BH4; 2; 1.
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PROSITE;
PROSITE;
PROSITE;
PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                        Submitted (MAY-2001) to the EMBL; AL160175; CAC10003.1; HSSP; Q07817; LLXL.
                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TIEMBLrel. 16, Created)
01-MAR-2001 (TIEMBLrel. 16, Last sequence update)
01-DEC-2001 (TIEMBLREL. 19, Last annotation update)
BA243316.1.1 (BCL2-LIKE 1 (ISOFORM 1)) (FRAGMENT)
BCL2L1.
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                              Brown
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9H1R6;
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                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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 66
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                                                                       11 RALVADFVGYKLRQKGY-----
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NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE
                       CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT
                                              RELYVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV
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                                                                                                 19; Conser
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; PS61080; BH1; 1.
;; PS61259; BH3; 1.
;; PS61260; BH4_1; 1.
;; PS61260; BH4_2; 1.
;; PS50063; BH4_2; 1.
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                                                                                                                                                                                                                                                                                                                                                         FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188
                                                                                                                                                             188 AA;
                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                  ; BH4_2; 1.
188
                                                                                                                                                           21029 MW; 7074B6095145C324 CRC64,
                                                                                              37.1%; Score 373.5; DB 4
42.9%; Pred. No. 2.2e-25;
Live 16; Mismatches 38
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           649D914C2D5378F6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                            Hominidae;
                                                                                                                     DB 4;
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                                                                          Length 188;
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Search completed: June 10, 2002, 10:31:19 Job time: 392 sec
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                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 83; Conserva
                                                                                                                                                                                                                                                                                                                                                     Nakajima K., Yaoita Y.;

"Muscle cell death occurs in the regressing tail of tadpole by suicide mechanism.";

Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AB055494; BAB62748.1;

EMBL; AB055494; BAB62748.1;

SEQUENCE 204 AA; 23189 MW; 1BEF1B904E29D84A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q90ZH2;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
BCL-XL
BCL-XL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopodinae; Xen
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q90ZH2
                                                                                               167
                                                                                                                           125
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                                                                    185 LLTI-VMLTGVFAL 197
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                                                                                                                                                                                                                                                            10 TRALVADFVGYKLRQ-----KGYVCGAGPGEGP----AADPLHQAMRA 48
                                                                                                                                                                                                                                  5 SRDLVEKFVSKKLSQNEACRKFSNNPQPNAISNGTSTSERPGEGATQGIVEEEVLQALLE
                                                                                                                                                                            WASVRTVLTGAVAL 180
                                                                                                                                         ESVNKEMEPLVGQVQEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLRE--GN 166
                                                                                                                                                                                          AGDEFETRERRIFSDLAAQLHVTPGSAQQRETQVSDELFQGGPNWGRLVAFFVFGAALCA 108
                                                                                                                        ESANKEMTDLLPRIVQWMVNYLEHTLQPWMQENGGWEAFVGLYGKNAAAQSRESQERFGR 184
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus.
                                                                                                                                                                                                                                                                                      37.0%; Score 373; DB 13; Length 204; 42.8%; Pred. No. 2.7e-25; tive 24; Mismatches 63; Indels 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204 AA
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Minimum DB seg length: Maximum DB seg length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
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                                                                                                                                                                                                                                                                                                                                                                           NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maximum Match 100%
Listing first 45 summaries
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99.3
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                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                              DB
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                             AAY05531

AAW61391

AAW97393

AAY05530

AAW61392

AAW61392

AAW36047

AAW36047

AAW36047
                                                                                                                                                                                                                     Mouse Bcl-w protein.
Rat bcl-y protein.
The rat bcl-y prot
Protein sequence o
                                                                                                                                                                                                                                                                                                                                                                                 Description
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Apoptosis-blocking		17	232	0	404
		22	485		406.5
Human DC12		19	272	•	406.5
Human BC1-2		22	239		406.5
Human BCL-2		22	239		406.5
Human bc1-2alpha.		22	239	•	406.5
Human Bc1-2		22	239	•	406.5
Human Bc1-2	AAG64035	22	239	40.3	406.5
Human Bc1-2		22	239		406.5
A human Bcl-		20	239		406.5
Human bcl-2.		19	239		406.5
Human bc1-2 al		16	239		406.5
Human bcl-2		16	239	0	406.5
Bc1-2 oncoge		14	239	0	406.5
ce of bc1-	AAP809	9	239		406.5
٠.		22	239		408.5
Human bcl-2.		22	239	•	408.5
A human Bcl-2		20	239	40.5	408.5
Murine Bcl-2.		22	236		4
Human Bc1-2 pro		22	239		7
Mutant rat BC1-xL		22	233	41.8	421.5
"Deprenyl"		18	225	•	422
Protein encoded b	AAB47515	22	233	42.1	4
Human Bcl-xL pr		22	233	42.1	424.5
Human Bcl-XL		22	233	42.1	4
Human Bcl-XL		21	233	٠	24.
Bcl-x polyper		21	233	•	24.
Human		18	233	•	4
Bcl-XL		17	233	42.1	4
Human thymus BCL-X	AAR68	16	233	•	
Rat wild-type Bcl-	AAB7330	22	233	•	ა
		22	411	42.6	9
cid	AAW5988	19	365	4	S.
Mouse bcl-w protei	AAW36048	18	168	•	7

### ALIGNMENTS

#### AAY05531 Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility; Mouse Bcl-w protein essential for spermatogenesis. 05-JUL-1999 (first entry) AAY05531 standard; Protein; 193 AA Mus sp. animal model WPI; 1999-243890/20. N-PSDB; AAX25133. WO9913710-A1 Adams J, Cory S, Gibson L, 16-SEP-1997; 16-SEP-1998; 25-MAR-1999. (HALL-) HALL INST MEDICAL RES WALTER & ELIZA. \_ 97AU-0009228. 98WO-AU00764 Koentgen F, Print C;

193 193 193 193 193 193 193 193

20 20 20 20 20 20 20 20 20

Human Bcl-w protei Human bcl-y protei The human bcl-w protei Human bcl-w protei Human Bcl-w protei Mammalian bcl-y pr Mouse Bcl-w protei

Claim 2; Page 35; 52pp; English

protein associated with Bcl-w

An animal model exhibiting reduced levels of a Bcl-w protein and/or

AAY05533

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RESULT
AAW61391
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Nucleic acids encoding B-cell lymphoma-y protein - useful for
                               N-PSDB;
                                WPI; 1998-446079/38.
N-PSDB; V283333.
                                                                        Guastella
                                                                                                                           23-FEB-1996;
11-FEB-1997;
                                                                                                                                                                   11-FEB-1997;
                                                                                                                                                                                              04-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      molecules and genetic sequences useful for inducting or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce
                                                                                                (COCE-) COCENSYS INC
                                                                                                                                                                                                                       US5789201-A
                                                                                                                                                                                                                                                 Rattus sp.
                                                                                                                                                                                                                                                                                                    Rat bcl-y protein
                                                                                                                                                                                                                                                                                                                                02-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                  AAW61391 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infertility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is mouse Bcl-w, a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 GALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MATPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \verb|matpastpdtralvadfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fs \tt dlaaqlhvtpgs aqqrftqvs delfqggpnwgrlvaffvfgaalcaes vnkemeplvg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                      ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 AA;
                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                      cell death pathway; apoptotic; apoptosis; rat.
                                                                                                                          96US-0012201.
97US-0798897.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to an animal model for the identification of
                                                                                                                                                                   97US-0798897
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                                                                                                                                                                                                                                                                                                                                                                                   193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1006; DB 20;
Pred. No. 5.5e-102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 193;
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                                                                        23-FEB-1996;
11-FEB-1997;
25-NOV-1997;
             Guastella J;
                                                                                                                                                                                                                                                                                     Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span;
                                                                                                                                                                                                   US5883229-A
                                                                                                                                                                                                                               Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                   The rat bcl-y protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW97391;
                                         (COCE-) COCENSYS INC
                                                                                                                                    25-NOV-1997;
                                                                                                                                                                    16-MAR-1999
                                                                                                                                                                                                                                                               parasite.
                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW97391 standard; Protein; 193 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The mammalian bcl-y protein is a member of the bcl-2 family, components in the cell death pathway. The bcl-2 family have both apoptotic activit and the apoptosis blocking activity. bcl-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Als antisense constructs can be used in disorders where prevention of cell
                                                                                                                                                                                                                                                                           Kaposi's sarcoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       producing recombinant protein for use in treating uncontrolled cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 FSDLAAQLHVTPGSAQQRETQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MATPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \verb|matpastpdtralvadfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         desired.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          193 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancers
                                                                      96US-0012201.
97US-0798897.
97US-0978523.
                                                                                                                                   97US-0978523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.3%;
                                                                                                                                                                                                                                                                             cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1002; DB 19;
Pred. No. 1.5e-101;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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RESULT
AAM97393
ID AAM9
AC AAM9
AC AAM9
AC AAM9
XX 20-M
XX 20-M
XX Prot
XX Prot
XX Rat
KW Prog
KW head
KW head
KW mult
KW agiin
KW prem
KW Kap
KW parz
XX Unic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents rat bcl-y protein (Rbcl-y). The grecification also describes human bcl-y protein (Hbcl-y). Rbcl-y and CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y cc proteins may be used to treat conditions associated with a disruption of cc the cell death pathway. If they act as cell death inhibitors, they may be used in therapies to treat subjects suffering from: strokes, head trauma, and the conditions associated with a disruption of cc last death, aging, spinal cord injuries and amyotrophic lateral cc cell death, aging, spinal cord injuries and amyotrophic lateral as a cresult of triggers which may or may not be apparent. They may also be used in this way to develop cell lines which remain viable in culture for can extended period. In contrast, if they act as cell death stimulators, can extended period. In contrast, if they act as cell death stimulators and duto/hyperimmune diseases. They may also be used to creat conditions associated with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel bcl-y homologues of the rat and human bcl-2 protein \, - useful for modulating programmed cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAX15945
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                                                                                                   programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                                                                                                                                                                                                                                                                  Protein sequence of the specification.
                                                                                                                                                                                                                                                                                                                              20-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                   AAW97393 standard; Protein; 192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cause cell death in, and hence control, parasites.
                                           Unidentified
                                                                                                                                                                                                                  rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 GALVTVGAFFASK 193
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Pred. No. 1.5e-101;
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RESULT
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XEXEXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local (
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11-FEB-1997;
25-NOV-1997;
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                                                                                                                                                                                                                                                                       AAY05530;
                                             Human Bcl-w protein essential for spermatogenesis.
                                                                                                                                                          05-JUL-1999
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97US-0798897.
97US-0978523.
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Pred. No. 5.3e-101;
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RESULT
AAW61392
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Best Local
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                   02-OCT-1998
                                                     AAW61392;
                                                                                    AAW61392 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is human Bcl-w, a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of the formal sequences are provided for the treatment of the sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An animal model exhibiting reduced levels protein associated with \ensuremath{\mathsf{Bcl-w}}
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                                                                                                                                                                                                                                    qvqewmvayletrladwihssggwaeftalygdgaleearrlregnwasvrtvltgaval
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DB; AAX25132.
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98.4%;
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Pred. No. 5.3e-101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
       Rat bcl-y protein;
                                     The human bcl-y protein.
                                                                                                              AAW97392;
                                                                                                                                       AAW97392 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The mammalian bcl-y protein is a member of the bcl-2 family, component; in the cell death pathway. The bcl-2 family have both apoptosis activity and the apoptosis blocking activity, bcl-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. All antisense constructs can be used in disorders where prevention of cell death is decirated.
                                                                            20-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            death is desired.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding B-cell lymphoma-y protein - useful for producing recombinant protein for use in treating uncontrolled cell growth \mathbf{e}\cdot\mathbf{g}. cancers
                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                          Example; Column 17/18; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-FEB-1996;
11-FEB-1997;
                                                                                                                                                                                                                               181 galvtvgaffask 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (COCE-) COCENSYS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US5789201-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human bcl-y protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hes 189;
                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MATPASTPDTRALVADFVGYRLROKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT
                                                                                                                                                                                                                                                                   GALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                    matpasapdtralvedfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1998-446079/38.
DB; AAV28334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96US-0012201.
97US-0798897.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0798897
Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98.3%;
97.9%;
                                                                                                                                             193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 992; DB 19;
Pred. No. 1.9e-100;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 193;
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Query Match
Best Local
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11-FEB-1997;
25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the cell death pathway. If they act as cell death inhibitors, they may be used in therapies to treat subjects suffering from: strokes, head trauma, Alzheimer's Disease, neural and muscular degenerative diseases (especially multiple sclerosis), myocardial infarction, vitally induced cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis- conditions where cells under go premature cell death as a result of triggers which may or may not be apparent. They may also be used in this way to develop cell lines which remain viable in culture for an extended period. In contrast, if they are that conditions associated with prolonged cell life span such as cancer (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune diseases. They may also be used to cause cell death in, and hence control, parasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5883229-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents human bcl-y protein (Hbcl-y). The specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein thought to be involved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Columns 17-18; 26pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guastella J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  parasite.
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proteins may be used to treat conditions associated with a disruption of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for modulating programmed cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (COCE-) COCENSYS INC
                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>,_</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MATPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1999-214150/18
FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  matpasapdtralvedfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt
                                                                                                                                                                                                                                                                                                                              QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL
                                                                                                                   GALVTVGAFFASK 193
                                                                                                                                                                                                                \tt qvqewmvayletrladwihssggwaeftalygdgaleearrlregnwasvrtvltgaval
                                                                                                                                                                                                                                                                                                                                                                                                                                      fsdlaaqlhvtpgsaqqrftqvsdelfqggpnwgrlvaffvfgaalcaesvnke meplvggrapher and the statement of the statement of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-0012201.
97US-0798897.
97US-0978523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0978523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.3%;
97.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 992; DB 20;
Pred. No. 1.9e-100;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful
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                                                                                                                                                                                                                                                                                                                                               180
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                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                               This sequence represents a novel human protein, bcl-w, encoded by the bcl-2 gene family and extracted from an adult brain library. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Upregulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosis; degenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human bcl-w protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW36047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW36047 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Page 48; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid encoding apoptosis related gene bcl-w - used or inhibit cell survival, e.g. for treatment of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-OCT-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adams JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AMRA-) AMRAD OPERATIONS PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAR-1996;
                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     degenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                      antibody production or screening of potential modulators
 181
                          181
                                                      121
                                                                                  121
                                                                                                             61
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                                                                                                                                                                               1 MATPASTPDTRALVADFVGYRLROKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
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galvtvgaffask 193
                                                                   QVQDWMYAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                                                                               FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                               \verb|matpasapdtralvadfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1997-489635/45.
              GALVTVGAFFASK 193
                                                      \tt qvqewmvayletrlvdwihssggwaeftalygdgaleearrlregnwasvrtvltgaval
                                                                                                           188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT96577
                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cory S,
                                                                                                                                                                                                                                                                                             193
                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gibson LM, Holmgreen SP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                      98.1%;
97.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193
                                                                                                                                                                                                                                       Score 990; DB 18;
Pred. No. 3.1e-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                   Length 193;
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AAY05532
                                                                                                                                                                                                                                                                                                                               The present sequence is described of a derivative of human Bcl-w (see also AAV(0530), a pro-survival member of the Bcl-2 family that is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to
                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                            screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce infertility.
                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          An animal model exhibiting reduced levels of a Bcl-w protein and/or
 181
                             121
                                                      121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HALL-) HALL INST MEDICAL RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spermatogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Bcl-w protein essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY05532 standard; Protein; 193 AA.
                                                                                    61
                                                                                                              61
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                                                                                                                                                 1 MATPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                           GALVTVGAFFASK 193
                                                  QVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180
                                                                                                                                   \verb|matpasapdtralvadfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrt|
                         qvqewmvayletrlvdwihssggwaeftalygdgaleearrlregnwasvrtvltgaval
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens
                                                                                                                                                                                                  188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  associated with Bcl-w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cory S,
                                                                                                                                                                                                                                                                    193 AA;
                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-AU00764.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bcl-3; Bcl-2; human; fertility; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gibson L,
                                                                                                                                                                                                            98.1%;
97.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52pp; English.
                                                                                                                                                                                                 ω
••
                                                                                                                                                                                                           Score 990; DB 20;
Pred. No. 3.1e-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Koentgen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WALTER & ELIZA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for spermatogenesis
                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Print C;
                                                                                                                                                                                                                        Length 193;
                                                                                                                                                                                              Indels
                                                                                                                                                                                              0;
                                                                                                                                                                                           Gaps
                                                                                                        120
                                                                                                                                      60
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The present sequence represents a mammalian boy-1 protein.

C. The specification describes rat bol-y protein (Rbcl-y) and human bcl-y protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein (thouse). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein concentration of the cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y proteins may be used to treat conditions associated with a disruption of the cell death pathway. If they act as cell death from: strokes, head trauma, Alzheimer's Disease, neural and muscular degenerative diseases (especially multiple sclerosis), myocardial infarction, vitally induced cell death, aging, spinal cord injuries and amyotrophic lateral sclerosis- conditions where cells under go premature cell death as a result of triggers which may or may not be apparent. They may also be used in this way to develop cell lines which remain cell cell death as in culture for an extended period. In contrast, if they act as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW97394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
                             viable in culture for an excended period. In concern cell death stimulators, Rbcl-y and Hbcl-y may be used to treat conditions associated with prolonged cell life span such as cancer (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune diseases. They may also be used to cause cell death in, and hence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-FEB-1996;
11-FEB-1997;
25-NOV-1997;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Columns 19-22; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel bcl-y homologues of the rat and for modulating programmed cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-214150/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (COCE-) COCENSYS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5883229-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     parasite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalian bcl-y protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW97394 standard; Protein; 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-MAY-1999
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AA;
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97US-0798897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human bcl-2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful
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Query Match
Best Local Similarity
Matches 188; Conserv

Conservative

97.8%; 97.9%;

Score 987; DB 20; Pred. No. 6.6e-100; 2; Mismatches 2;

Length 192; Indels

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Gaps

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                                                                                       animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene associated with bcl-w. Such animals have disorganised seminferous tubules and are substantially infertile, but possess no other major abnormalities
Sequence
                              as determined by histological examination. They can be used screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce infertility.
                                                                                                                                                                                                                      The present sequence is described of a derivative of mouse Bcl-w (see also AAY05531), a pro-survival member of the Bcl-2 family that is widely expressed and which is essential for spermatogenesis. The derivative lacks the 24 N-terminal amino acids of Bcl-w. The invention relates generally to a method of treatment and to an
                                                                                                                                                                                                                                                                                                                        Disclosure; Page 39; 52pp; English
                                                                                                                                                                                                                                                                                                                                                                      An
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adams
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spermatogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse Bcl-w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                      animal model exhibiting reduced levels otein associated with Bcl-w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    {\tt atpasapdtralvedfvgyklrqkgyvcgagpgegpaadplhqamraagdefetrfrrtf}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRERRTF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALVTVGAFFASK 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      {\tt sdlaaqlhvtpgsaqqrftqvsdelfqggpnwgrlvaffvfgaalcaesvnkemeplvgq}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQ 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cory S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein deritvative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bcl-3; Bcl-2; mouse; fertility; infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gibson L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Koentgen F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WALTER & ELIZA.
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                                                                                                                                                                                                                                                                                                                                                                      Bcl-w protein and/or
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AAW36048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 186;
                                   This sequence represents a novel protein, bcl-w, encoded by the mouse bcl-2 gene family. This gene promotes cell survival, so its modulation is useful in treatment of cancer or auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia, human immunodeficiency virus infection or in cell transplants. Up-regulation of the gene can also be used to modify cell lines cultured in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas and to increase survival of primary explants during genetic modification. It can be used to produce recombinant Bcl-w for therapy, diagnosis, antibody production or
                                                                                                                                                                                                                 Nucleic acid encoding apoptosis related
or inhibit cell survival, e.g. for treat
degenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW36048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW36048 standard;
                                                                                                                                                                                        Claim 6; Page 50-51; 86pp; English.
                                                                                                                                                                                                                                                                         WPI; 1997-489635/45.
N-PSDB; AAT96578.
                                                                                                                                                                                                                                                                                                                 Adams JM,
                                                                                                                                                                                                                                                                                                                                                                    27-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                27-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse bcl-w protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-APR-1998
Sequence
                           screening
                                                                                                                                                                                                                                                                                                                                        (AMRA-) AMRAD OPERATIONS PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MATPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mptpastpdtralvadfvgyrlrqkgyvcgagpgegpaadplhqamraagdefetrfrrt 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fs dlaaq lhvtpg saqqrftqvs delfqggpn wgrlvaffvfgaal caes vnkemeplvg~120 \\
                                                                                                                                                                                                                                                                                                              Cory S,
                           of potential modulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        degenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                                                                                                                                                                 Gibson LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96.2%;
                                                                                                                                                                                                                                ptosis related gene e.g. for treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 970.5;
Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ΑA
                                                                                                                                                                                                                                                                                                                Holmgreen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.2e-98;
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                                                                                                                                                                                                                                  bcl-w - used to of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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RESULT 1
AAMS 9884
ADW 59884
ID AAMS 9884
XX AAMS 9884
AC AAMS AC AAMS
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                                                                                                      Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotides and encoded polypeptides - used to develop products for treating e.g. inflammatory diseases, infections, immunological disorders, autoimmune diseases, allered
                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Feng
                                                                                                                                                                                                                                                     used for treating conditions associated with abnormal expression of the polypeptides. They can be used for e.g. treating chronic inflammatory diseases, immunological disorders, autoimmune diseases, inflammatory diseases, various allergies, and anti-infectious age
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 12A-12D; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
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21-JAN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction; immunological disorder; autoimmune disease; anti-infectious agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ( HUMA - )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-JUL-1998
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                                                                                                                                                                                                                                                products can also
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                                                                                                                                                                                                                                                                                                                                is the amino acid sequence of the cDNA clone Bcl-like (HAICH29), in the method of the invention. The products of the clone can be for treating conditions associated with abnormal expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1998-414099/35
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                                                                                                      Similarity
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97US-0034204.
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97.98;
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                                                                        Pred. No. 3.26
2; Mismatches
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3.2e-74;
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                                                                                                                                                                                                                                                                                  Novel fusion protein for modifying apoptosis in target cell and reducing apoptosis after transient ischaemic neuronal injury, he domain, which targets protein to a cell and modifies apoptotic:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Youle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-AUG-1999;
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diphtheria toxin receptor binding domain; DTR; neoplasm; tumour; hyper-proliferation; Alzheimer's disease; neurodegenerative disorder; transient ischaemic neuronal injury; stroke; spinal cord injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (USSH)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bcl-Xl-DTR; apoptosis; cancer; spinal muscular atrophy;
                                                                                                                                                                                                                                                                                                                                                                                              AAS00247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "DTR, diphtheria toxin receptor binding domain"
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The sequence represents the amino acid sequence of Bcl-Xl-DTR apoptosis-modifying fusion protein comprising Bcl-Xl sequence fused via a short linker to diphtheria toxin receptor binding domain (DTR). The functional apoptosis-modifying fusion protein is capable of binding a target cell and integrating into or crossing a cellular membrane of the target cell. comprising at least two domains, one of which targets the fusion protein to the target cell and another of which modifies an apoptotic response of the target cell and another of which modifies an apoptotic response of the target cell and another of which modifies an apoptotic response of the target cell and another of which modifies an apoptotic response of the target cell and another of which modifies an apoptotic response of the target cell and another of which modifies and apoptotic response of the target cell and another of which modifies and apoptotic response of the target cell and another of which modifies and apoptotic response of the target cell and another of which modifies and apoptotic response of the target cell and another of which modifies and apoptotic response of the target cell and another of which modifies and apoptotic response of the target cell and another cell another cell and another cell and another cell and another cell another cell and another cell and another cell and another cell another cell and another cell and another cell and another cell another cell and another cell another cell and another cell anot Claim 4. Page cell. 56-57; 65pp; The fusion English. protein is useful

cell and modifies apoptotic response

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             Modified cDNA of rat bcl-x gene and encoded protein with membrane permeability to enhance uptake for effective inhibition of cell deat. e.g. apoptosis, useful in remedies for diseases associated with cell death -
                                                                                                                                            Ohta
                                                                                                                                                                                                                                                                                                                                                                                      Rat Bcl-xL; apoptosis inhibitor; programmed cell death inhibitor;
wild-type; antiapoptotic; cell death-associated disease;
                                                                                                                                                                           (NISC-) JAPAN SCI & TECHNOLOGY CORP
                                                                                                                                                                                                            17-AUG-1999;
                                                                                                                                                                                                                                         17-AUG-2000; 2000WO-JP05502
                                                                                                                                                                                                                                                                         22-FEB-2001
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                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat wild-type Bcl-xL protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 relvvdflsyklsqkgyswsqfsdveenrteapegtesemetpsaingnpswhladspav 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS 141
                                                                                                                                            ູດ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ggwdtfvelygnnaaaesrkgqerfnrwfltgmtvagvvllgslfsrkaysaa 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGALVTVGAFFAS 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ngatahss \verb|sldarevipmaavkqalreagdefelry| rrafsdltsqlhitpgtayqsfeq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                                                                                             2001-211219/21.
DB; AAF75960.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                            Asoh S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                411 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                            99JP-0230642
                                                                                                                                                                                                                                                                                                                                                                       preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.6%; Score 429.5; DB 22;
39.5%; Pred. No. 2.1e-38;
39.5%; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GEGPAA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145
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Best Local
                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein. The invention also encompasses recombinant vectors and host cells comprising the modified nucleic acid sequence. The mutant Bcl-x protein is able to permeate the cell membrane, thus enhancing its ability to be taken up into a cell and to act as an inhibitor of apoptosis (programmed cell death). Bcl-xFIX and nucleic acids encoding it are useful in remedies for diseases associated with cell death and in additives for maintaining the stability of transplanted cells and organs. The present sequence represents wild-type rat Bcl-xL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a mutant rat Bcl-x protein and the cDNA encoding it. The mutant rat Bcl-x protein (Bcl-xFNK) has the substitutions Y22F, Q26N, and R165K relative to the wild-type Bcl-xL substitutions Y22F, Q26N, and R165K relative to the wild-type Bcl-xL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6; Page 45-46; 56pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                         141
                                                                                  125
                                                                                                                          81
                                                                                                                                                                   99
                                                                                                                                                                                                          29
                                                                                                                                                                                                                                                                                           11 RALVADFVGYRLRQKGY-----V 28
                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 92; Conserv
                                                                                                                                                                                                                                                    σ
                                                                                                                                                                                       CGAGPGEGPAAD------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
                            SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                                relvvdflsyklsqkgyswsqfsdveenrteapeeteperetpsaingnpswhladspav 65
nggwdtfvdlygnnaaaesrkgqerfnrwfltgmtvagvvllgsl 229
                                                                                                                       QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
                                                                                                                                                               nga-tghsssldarevipmaavkqalreagdefelryrrafsdltsqlhitpgtayqsfe 124
                                                                                                                                                                                                                                                                                                                                                                                                                                           233 AA;
                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                          42.2%;
                                                                                                                                                                                                                                                                                                                                       23; Mismatches
                                                                                                                                                                                                                                                                                                                                Score 425.5; DB 22;
Pred. No. 2.7e-38;
""" matches 57;
                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                     Gaps
```

4.

Search completed: June 10, 2002, 10:25:48 Job time: 161 sec

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OM protein - protein search, using sw model
                                                                                  GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
```

June 10, 2002, 10:26:22; Search time 28.15 Seconds (without alignments) 658.801 Million cell updates/sec

Title: Perfect score:

Sequence: US-09-155-327E-9 1009 1 MATPASTPDTRALVADFVGY.....LTGAVALGALVTVGAFFASK 193

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

				25	24		22	21	20	19	18 2	17			14 3		12			9	80			υ		3 4	2 4	1 4	Result No. S
	147.5	150.5	154	154	154	158.5	169	171	174	179	77.5	342	345.5	353	371.5	374.5	375	399	401.5	402	403	408	408.5	4	2	421.5	4	G	Score
	14.6	14.9	15.3	15.3	15.3	15.7	16.7	٠					34.2		36.8	7.	.7	9	9	9.	39.9	0		0	41.7		٠	42.2	Query Match ]
	179	133	280	261	192	192	211	176	211	170	154	205	199	216	227	214	190	236	233	236	236	236	239	232	233	233	233	233	Length
J	N	N	N	ν	N	2	N	N	2	N	N	-	Н	Ν	N	N	N	2	Ν	_	N	N	$\vdash$	2	N	N	N	N	DB B
	JC7255	I53295	A53189	н88578	A47538	D47538	S58875	167435	S58873	I49055	I58194	TVHUB1	TVMSB1	в37332	JE0203	I49057	A47537	JC7383	167431	TVMSA1	I53744	167432	TVHUA1	S24390	A37332	S51761	B47537	I49056	Ħ
, he - 1	Bax-c	bc1-2	apopt	prote	bc1-2	bc1-2	cdn-2	gene	Bak p	bcl-x	gene	trans	trans	trans	apopt	bcl-x	apopt	B-cell	BCL-X	trans	gene	BCL-2	trans	trans	trans	BCL-X	apoptosis	bcl-x	Descr
`	Bax-delta protein	bcl-2-associated	apoptosis suppres	protein ced-9	2-associated	- 1	2 protein -	р	protein -	short	bcl-2 protein	transforming	transforming	μ.	apoptosis regulato	bcl-x transmembran	apoptosis regulato	ll lymphoma	BCL-X-Long - rat	5	gene bcl-2 protein	$\overline{}$	transforming prote		transforming prote	$\overline{}$	cosis regulato	long	Description

RESULT 2
B47537
B47537
Apoptosis regulator bcl-xL - human
Apoptosis regulator bcl-xL - human
N; Alternate names: bcl-2-related protein

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
81.5	82.5	83.5	83.5	83.5	86	86	86.5	86.5	88	105	116	119	138.5	141	144
8.1	8.2	8.3	8.3	8.3	8.5	8.5	8.6	8.6	8.7	10.4	11.5	11.8	13.7	14.0	14.3
886	3430	872	872	358	279	270	3433	301	185	172	350	175	143	255	177
2	1	Ν	N	۲	N	N	۳,	2	N	N	N	N	N	N	2
A32758	GNWVWV	G98026	н95160	AJLCQB	B97381	AI2598	GNWVKV	T36534	в83217	I49449	A47476	I39055	138921	JC7567	S54778
beta-amyloid-like	genome polyprotein	alaninetRNA liga	alanyl-tRNA synthe	glutamateammonia	dihydrodipicolinat	dihydrodipicolinat	genome polyprotein	probable lipase/es	hypothetical prote	hemopoietic-specif	BCL2 homolog MCL1	Bcl-2 related - hu	bcl-2-associated p	Mcl-la protein - z	NR-13 protein - qu

## ALIGNMENTS

A;Status: preliminary A;A;Status: preliminary A;A;Molecule type: mRNA A;Residues: 1-233 <kam> A;Residues: 1-233 <kam> A;Residues: 1-233 <kam> A;Cross-references: EMBL:X83574; NID:g695622; PIDN:CAA58557.1; PID:g695623 C;Superfamily: bcl transforming protein  Query Match Best Local Similarity 40.9%; Pred. No. 4.3e-32; Matches 92; Conservative 23; Mismatches 57; Indels 53; Gaps 4; Matches 92; Conservative 23; Mismatches 57; Indels 53; Gaps 6  [</kam></kam></kam>	RESULT 1 149056 bcl.x long - mouse C;Species: Mus musculus (house mouse) C;Decies: Mus musculus (house mouse) C;Decies: Mus musculus (house mouse) C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999 C;Accession: I49056; S52866 C;Accession: I49056; S52866 R;Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W. J. Immunol. 153, 4388-4398, 1994 A;File: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes A;File: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes A;Reference number: I49055; MUID:95052604 A;Recession: I4905 A;Residues: 1-233 <res> A;Residues: 1-233 <res> A;Residues: 1-233 <res> A;Cross-references: EMBL:U10101; NID:9506647; PIDN:AAA82173.1; PID:9506648 A;References: EMBL:Undid: N.Y.; Takatsu, K.; Okuma, M. Submitted to the EMBL Data Library, November 1994 A;Reference number: S52866 A;Recession: S52866</res></res></res>
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submitted to the EMBL Data Library, A; Reference number: S51761 A; Accession: S51761
                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-125,189-233 <MI2>
A;Cross-references: EMBL:X82537; NID:g607176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BCL-X protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 02-Mar-2001
C;Accession: S51761; S51762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N;Contains: apoptosis regulator bcl-xs (;Species: Homo sapiens (man) (;Species: homo sapiens (ma
    A; Introns:
C; Superfam
                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: embryonic; brain A; Accession: S51762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-233 <MIC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        망
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C;Keywords: alternative splicing; apoptosis
F;1-233/Product: apoptosis regulator bcl-xL #status predicted <MAT>
F;1-125,189-233/Product: apoptosis regulator bcl-xS #status predicted
                                                                                                                          A; Note: smaller form due to
                                                                                                                                                                          A; Experimental source:
                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X82537; NID:g607176; PIDN:CAA57886.1; PID:g607177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Michaelidis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: GDB: BCL2L
A; Cross-references: GDB: 228079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-69,'G',71-125,189-233 <BO2>
A;Cross-references: GB:L20122; NID:g623236; PIDN:CAA80662.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:L20121; NID:g510900; PIDN:CAA80661.1; A;Accession: C47537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: B47537
A;Status: nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptoti A; Reference number: A47537; MUID:93364977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: nucleic acid sequence not shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 90
        Superfamily:
                                                                                       Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 VVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEFWIQEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NGATAHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65
                                       125/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1-233 <BOI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
bcl transforming
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                      embryonic; brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.1%; Score 424.5; DB 2;
40.2%; Pred. No. 5.3e-32;
tive 24; Mismatches 59;
                                                                                                                               splicing
protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 November 1994
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                                                                                                                                                                                                                  PIDN: CAA57887.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----VCGAGP----GEGPAA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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A;Introns: 189/3
C;Superfamily: bcl transforming protein
C;Keywords: mitochondrion; transforming protein; transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transforming protein (bcl-2-alpha) - chicken

(;Speciles: Gallus gallus (chicken)

C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 23-Feb-1997

C;Accession: A37332; S35453

C;Accession: A37332; S35453

R;Eguchi, Y; Ewert, D.L.; Tsujimoto, Y.

Nucleic Acids Res. 20, 4187-4192, 1992

A;Title: Isolation and characterization of the chicken bcl-2 gene: expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
A37332
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C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Вb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-233 <EGU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A37332; MUID:92375724 A; Accession: A37332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      뫄
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Best Local
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                                     145
                                                                             130
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190 DAFVELYGN----SMRPLFDFSWISLKTILS-LVLVGACITLGAYLGHK 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143
                                                                                                                                                                                                                                                                                                                                     y Match 41.7%; Score 420.5; DB 2 Local Similarity 37.6%; Pred. No. 1.3e-31;
                                                                                                                  85
                                                                                                                                                                                                  42
                                                                                                                                                                                                                                       10
                                                                                                                                                          70 AASEVPPAEGLRPAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTAHGRFVAVVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83
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                                                                                                                                                                                                                                                                               9 DTRALVADFVGYRLRQKGYVCGAG-----PGEGPAADP------
                                   AEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEFWIQENG
                                                                             ELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGW
                                                                                                                                                                                                                                       DNREIVLKYIHYKLSQRGYDWAAGEDRPPVPPAPAPAAAPAAVAAAGASSHHRPEPPGSA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GWDTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGPGEGPAAD-----
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                                                                                                                  ELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGW 144
                                                                                                                                                                                                SDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91;
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                                                                                                                                                                                                                                                                                                                33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 421.5; DB Pred. No. 1e-31;
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                                                                                                                                                                                                                                                                                                                                                        DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56;
                                                                                                                                                                                                                                                                                                                                                      Length
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                                                                                                                                                                                                                                                                                                                     49;
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                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                               189
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transforming protein (Bcl-2) homolog - chicken C;Species: Gallus gallus (chicken) C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change

C; Accession: S24390 R; Cazals-Hatem, D.L.;

Biophys.

Acta

; Louie, ta 1132,

D.C.; Tanaka, 109-113, 1992

s.;

16-Jul-1999

S24390

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R.Tsujimoto, Y.; Croce, C.M.

R. Reference number: A29409

R. Reference number: A29409; MUID:86259760

R. Reference in RNA

R. Residues: 1-95, 'A', 97-109, 'G',111-236,'S', 238-239 <TSU>
R. R. Residues: 1-95, 'A', 97-109, 'G',111-236,'S', 238-239 <TSU>
R. R. Residues: 1-95, 'A', 97-109, 'G',111-236,'S', 238-239 <TSU>
R. R. Residues: 1-95, 'A', 97-109, 'G',111-236,'S', 238-239 <TSU>
R. R. Residues: 1-95, 'A', 97-109, 'G',111-236,'S', 238-239 <TSU>
R. R. Seto, M.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett, S.; Goldman, Rubbo J. 7, 123-131, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C:Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 07-Jun-1996 #text_change 15-Oct-1999
C;Accession: C37332; A29409; S02452; A24428; A27622; B27622
R;Eguchi, Y:; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expressic A;Reference number: A37332; MUID:92375724
A;Accession: C37332
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A;Recession: S24390
A;Status: preliminary
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: nucleic acid sequence not shown;
A;Molecule type: DNA
A;Residues: 1-239 <EGU>
A;Note: this report is a correction
R;Tsujimoto, Y.; Croce, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
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A; MoLecule type: mRNA
A; Residues: 1-58,'T','60-116,'R',118-239 <CLE>
A; Cross-references: GB:M14745; NID:g179370; PIDN:AAA35591.1; PID:g179371
R; Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Wright, J.J
Oncogene Res. 2, 263-275, 1988
                                                                                                                                           R:Cleary, M.L.; Smith, S.D.; Sklar, J.
Cell 47, 19-28, 1986
A;Title: Cloning and structural analysis of cDNAs
A;Reference number: A24428; MUID:87002488
A;Accession: A24428
                                                                                                                                                                                                                                                                                                                                                   A; Title: Alternative promoters and exons, A; Reference number: S02452; MUID:88196071 A; Accession: S02452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:Z11961; NID:g62969; PIDN:CAA78018.1; C;Superfamily: bcl transforming protein
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                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-239 <SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transforming
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Best Local S
Matches 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LFRDGVNWVRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGWD 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNREIVLKYIHYKLSQRGYDWAAGEDRPPVPPAPAPAAAPAAVAAAGASSHHRPSPPARL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DTRALVADFVGYRLRQKGYVCGAG-----PGEGPAADP------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein bcl-2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Pred. No. 9.5e-31;
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                                                                                                                                                                                                                                                                                                                                                                                                                   somatic
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                                                                                                                                                                                                                                                                                                                                                                                                                   mutation
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                                                                                                                                                                                                              and a hybrid bcl-2/immunog
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                                 J.J.; Bakhshi,
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82 70 28

VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS

141

81

SPLRPLVANAGPALSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129 -----VCGAGPGEGPAADPLHQAMRAAGDEFETRFRTFSDLAAQLHVTPGSAQQRFTQ

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A;Description: blocks apoptosis in hematopoietic cells C;Superfamily: bcl transforming protein C;Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma;
                                                                                                                                                                                                                                                                                                         R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L. Endocrinology 136, 232-241, 1995
A;Tille: Expression of members of the bcl-2 gene family in onstitutive bcl-2 and bcl-xlong messenger ribonucleic acid A;Reference number: I53295; MUID:95129487
                                                                                                                                                                                                                                                                                                                                                                                                              C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C:Accession: I67432
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A;Accession: A27622
Вþ
                                   Qy
                                                                                                                                                                                    A;Cross-references: EMBL:U34964; NID:g1004378; PIDN:AAA77687.1; PID:g1004379 C;Superfamily: bcl transforming protein
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A; Map position: 18q21.3-18q21.3
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A; Residues: 1-58, 'T', 60-239 < HUA>
                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-236 < RES>
                                                                                                                                                                                                                                                                      A; Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local :
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Best Local Similarity

    rat (fragment)

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DNREIVMKYIHYKLSQRGYEWDTGDEDSAPLRRAPTPGIFSFQPESNRTPAVHRDTAART
                                         DTRALVADFVGYRLRQKGY----
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                                                                                                     Score 408; DB 2;
Pred. No. 1.8e-30;
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R; Sato, T.;
Gene 140,
                                                      A:Cross-references: GB:L31532; GB:M16506; NID:g468336; PIDN:AAA37282.1; PID:g387109 R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y. Nucleic Acids Res. 20, 4187-4192, 1992 A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variance number: A37332; MUID:92375724 A:Accession: E37332
                                                                                                                                                                                                                 C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change
C;Accession: A25960; E37332
R;Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.
Cell 49, 455-463, 1987
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                A; Molecule type: DNA
A; Residues: 1-33, 'E'
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A; Residues: 1-236 <NEG>
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A; Residues: 1-236 <RES>
A; Cross-references: GB:L14680;
                                                                                                                                                                         A; Accession: A25960
                                                                                                                                                                                      A; Reference number: A90893;
                                                                                                                                                                                                     A; Title: Molecular analysis
                                                                                                                                                                                                                                                                                         transforming protein bcl-2-alpha - mouse
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;;Date: 29
                                        Status: preliminary; nucleic acid sequence not
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29-May 1998 #sequence_revision 29-May-1998
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                                                                                                                                                                                                                                                                                                                                                                GGWDAFVELYG----PSMRPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 236
                                                                                                                                                                                                                                                                                                                                                                                           GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                         VVEELFRDGVNWGRIVAFFEFGGVMCVGSVNREMSPLVDNIALWMTEYLNRHLHTWIQDN
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                                                                                                                                                                                                                                                                                                                                                  88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
85; Conser
                                                                                                                                                                                                                                                                                                                                                              Similarity
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B-cell lymphoma 2 protein - Chinese hamster C;Specles: Cricetulus griseus (Chinese hams: C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #sequence_revision: JC7383 R;Tomicic, M.T.; Christmann, M.; Kaina, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L. Endocrinology 136, 232-241, 1995
A;Title: Expression of members of the bcl-2 gene family onstitutive bcl-2 and bcl-xlong messenger ribonucleic ac A;Reference number: I53295; MUID:95129487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BCL-X-Long - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
C;Accession: 167431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Introns: 192/3
C;Superfamily: bcl transforming protein
C;Keywords: alternative splicing; mitochondrion; transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: bcl transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross references: EMBL: U34963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                              141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 RALVADFVGYRLRQKGY----
                                                                                                                                                                                                                                                                                                            QVVNELFRDGVNWGRIVASSSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE
                                                                                                                                                                                                                                                                                                                                                      QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
                                                                                                                                                                                                                                                                                                                                                                                                      NGA-TGHSSSLDAREVLPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTVYQSFE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWWYAYLETRLADWIHSS
                                                                                                                                                                                                                  NGGWDTFVDLYGNNTAPESRKGQERFNRWFLTGMTVAGVVLLGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEPERETPSAINGNPSWHLADSPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGWDAFVELYG----PSMRPLFDFSWLSLKTLLS-LPWVGACITLGAYLGHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNREIVMKYIHYKLSQRGYEWDAGDADAAPLGAAPTPGIFSFQPESNPMPAVHREMAART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DTRALVADFVGYRLRQKGYVCGAG-----PG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----EGPAADP----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.8%;
39.1%;
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36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 401.5; DB 2
Pred. No. 7.3e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 402; DB
Pred. No. 6.7e-
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                                                   hamster)
17-Nov-2000
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                                                #text_change
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                                                                                                                                                                                                                                                                183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53;
                                                   08-Dec-2000
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Biochem. Biophys. Res. Commun. 275, 899-903, 2000
A;Title: Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein.
A;Reference number: JC7383
A;Contents: Ovary
A;Accession: JC7383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Comment: \ This \ protein \ has \ anti-apoptotic function, and supports cell survival <math display="inline">C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-236 <TOM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: bcl transforming protein
C;Keywords: B-cell lymphoma; ovary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: bcl-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   apoptosis regulator bcl-x - chicken
C;Species: Gallus gallus (chicken)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 16-Jul-1999
C;Accession: A47537
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A;Residues: 1-190 <BOI>
A;Cross-references: GB:Z23110; GB:L20120; NID:g510898; PIDN:CAA80657.1; PID:g510899
C;Superfamily: bcl transforming protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A47537; MUID:93364977
A; Accession: A47537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 DNREIVMKYIHYKLSQRGYEWDVGDVDAAPLGAAPTPGIFSFQPESNPTPAVHRDMAART 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS 141
                                                                             126 LFHDGVNWGRIVAFFSFGGALCVESVDKEMRVLVGRIVSWMTTYLTDHLDPWIQENGGWV 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 SPLRPIVATTGPTLSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129
  186 R-TAL: 189
                                         146 EFTAL 150
                                                                                                                                                                                                                                                                                     9 DTRALVADFVGYRLRQKGY-----
                                                                                                                  86 LFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWA 145
                                                                                                                                                          66 VHRSSLEVHEIVRASDVRQALRDAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNE 125
                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                               6
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                                                                                                                                                                                                      -----AADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDE 85
                                                                                                                                                                                                                                             RELVIDEVSYKLSQRGHCWSELEEEDENRTDTAAEAEMDSVLNGSPSWHPPAGHVVNGAT 65
                                                                                                                                                                                                                                                                                                                                 80; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.5%; Score 399; DB 2; 34.9%; Pred. No. 1.3e-29;
                                                                                                                                                                                                                                                                                                                                                     37.2%; Score 375; DB 2; Length 190; 43.2%; Pred. No. 1.7e-27;
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                                                                                                                                                                                                                                                                                                                                       44; Indels
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                                                                                                                                                                                                                                                                                                                                            46; Gaps
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C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
C;Accession: I49057
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A;Accession: I49057
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: bcl-x-long C; Superfamily: bcl transforming protein
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A; Residues: 1-214 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes
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A;Title: Identification of a human cDNA encoding a novel bcl-x isoform. A;Reference number: JE0203; MUID:98340865
A;Accession: JE0203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 16-Jul-1999
C;Accession: JE0203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              apoptosis regulator bcl-x isoform - human N; Alternate names: h-bcl-xbeta
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C; Superfamily: b
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                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-227 <BAN>
QY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 RALVADFVGYRLRQKGY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 CGAGPGEGPAAD------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
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29 CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
                                                                                       11 RALVADFVGYRLRQKGY-----
                                                                                                                                                         Local Similarity
                                            6 RELYVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65
                                                                                                                                                                                                                                                 : 20
bcl transforming protein
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                                                                                                                                                         36.8%; Score 371.5; DB 240.3%; Pred. No. 4.3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17; Mismatches
                                                                                                                                         19;
                                                                                                                                           Mismatches 50;
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C;Species: Gallus gallus (chicken)
C;Decies: O3-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 24-Apr-1998
C;Accession: B37332; S35452
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a varie A;Reference number: A37332; MUID:92375724
A;Reference number: A37332; MUID:92375724
A;Accession: B37332
A;Status: nucleic acid sequence not shown
A;Roesule type: DNA
A;Residues: 1-216 <EGU>
A;Cross-references: EMBL:D11381; EMBL:D11382
C;Superfamily: bcl transforming protein
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                                                         145 AEFTA 149
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                                                                                                                                                                                                        10 DNREIVLKYIHYKLSORGYDWAAGEDRPPVPPAPAPAAAPAAVAAAGASSHHRPEPPGSA 69
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                                                                                                                                                                                                                                                                           / Match
Local Similarity 37.8%; Score 353; DB 2; Length 216;
Local Similarity 37.8%; Pred. No. 2.1e-25;
Nes 70; Conservative 22; Mismatches 49; Indels 44; Gaps
                                                                                                                                                                                                                                        9 DTRALVADFVGYRLRQKGYVCGAG------PGEGPAADP---------41
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Search completed: June 10, 2002, 10:26:22 Job time: 170 sec

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Result
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     BAKZ_HUMAN
BAXA_ROUSE
BAXA_HUMAN
CED9_CAEEL
BAXA_BOVIN
BAXB_HUMAN
NR13_COTJA
CED9_CAEBP
CAEBP
LUMAN
NR13_HUMAN
NR13_HUMAN
NR13_HUMAN
BAXD_HUMAN
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EAR_ASFB4
                                                                                                                                                                                                                                                                                                                                                                                                                       BCLW_MOUSE
BCLW_UMAN
AR1_XENLA
AR1_XENLA
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BCLX_PIG
BCLX_PIG
BCLX_RAT
BCLX_CHICK
BCL2_BOVIN
BCL2_BOVIN
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BCL2_MOUSE
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002718 bos taurus
p49950 rattus norv
p10417 mus musculu
p10415 homo sapien
09jiv8 cricetulus
091828 xenopus lae
008734 mus musculu
216611 homo sapien
013014 homo sapien
07813 mus musculu
063690 rattus norv
07812 homo sapien
207815 caenorhabdi
002703 bos taurus
007814 homo sapien
090343 coturnix co
p41957 caenorhabdi
052769 homo sapien
016548 homo sapien
017820 homo sapien
077819 african swi
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Q92843 homo sapien
Q91827 xenopus lae
Q07816 gallus gall
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9 gallus gall
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ry is copyright. I Institute of Bioin Ormatics Institute ormatics Institute institutions as tatement is not re license@isb-sib.c 056.1; 056.1; 86430.1; 1212. BGL2_family. ; BGL2_family. ; BGL2_f.	547 J. Clw Copl Oppl TO SSEE EE E	seq ann lata; lata; la; la; la; la; la; la; la; la; la; l	SQH POLL A4- POL POR YB4 YJ4- POL POL POL POL POL
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Q92843;
Q1-NOV-1997
                                                                             Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayasi Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.; "Prediction of the coding sequences of unidentified human The coding sequences of 80 new genes (KIAAO201-KIAAO200) danalysis of cDNA clones from cell line KG-1 and brain."; DNA Res. 3:221-329(1996).
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SEQUENCE
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                                                                                                                                                    MEDLINE=97191544; PubMed=9039502;
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01-NOV-1997 (Rel. 35,
16-OCT-2001 (Rel. 40,
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                           SEQUENCE FROM N.A.
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                                FUNCTION: PROMOTES CELL SURVIVAL.
SUBCELLULAR LOCATION: CYCOPLASMIC.
TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MYELOID CELL LINES
IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON
            AND SALIVARY GLAND DOMAIN: BH4 DOMAIN
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; PS01080; BH1; 1.
; PS01258; BH2; 1.
; PS01250; BH4_1; 1.
; PS50063; BH4_2; 1.
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MW; 36CA185F5945DFB4 CRC64;
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Pred. No. 1
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Q91827;
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PROSITE;
                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence updat
01-NOV-1997 (Rel. 35, Last annotation upo
Apoptosis regulator R1 (XR1) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/amor send an email to license@isb-sib.ch).
                                   Xenopodinae; Xen
NCBI_TaxID=8355;
                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM;
            SEQUENCE FROM
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InterPro; IPR003093; BH4.
InterPro; IPR000712; BC1_2.
                                                                                   kenopus laevis (African clawed
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PF02180; BH4; 1.
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Pred. No. 1.1e-81;
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Gene 158:171-179(1995).
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- I- BUYELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE PROPERTY OF MICHAEL STAGE OF SEVERAL FOLD HAS BEEN OBSERVED.
- ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.
- I- SIMILARITY: CONTAINS 1 ECL-2 HOMOLOGY DOMAIN 1 (BH1).
- I- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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HSSP; Q07817; 1MAZ.
InterPro; IPR002475; BCL2_family.
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PROSITE; PS01258; BH2; 1.
PROSITE; PS50062; BCL2_FAMILY; 1.
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                                                                               ECLX_CHICK STANDARD; PRT; 229 AA. 007816; Q98908; 01-FEB-1995 (Rel. 31, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [nterPro;
                                                                                                                                                                                                                            CHICK
                          Apoptosis regulator Bcl-X.
BCL2L1 OR BCLX OR BCL-X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105
                                                                                                                                                                                                                                                                                                                                      225
                                                                                                                                                                                                                                                                                                                                                                                                                                                165
                                                                                                                                                                                                                                                                                                                                                                                              190 FASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 TRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLH 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158:171-179(1995).
FUNCTION: COULD BE THE HOMOLOG OF MAMMALIAN BCL-W. conscentional (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pro; IPR000712; Bcl_2.
PF00452; Bcl-2; 1.
PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          LETNLRDWIQSNGGWNGFLTLYGDGAIEEARRQREGNWASLKTVLTGAVALGALWTVGAL 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VTPGTAYARFAEVAGSLFQGGVNWGRIVAFFVFGAALCAESVNKEMSPLLPRIQDWMVTY 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRALVEDLVRYKLCORSLV---PEPSGAASCALHSAMRAAGDEFEERFROAFSEISTQIH 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAY 129
                                                                                                                                                                                                                                                                                                                                      FASK 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SM00337; BCL; 1.
SM00265; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207
     (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139
186
227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25068 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 647.5;
Pred. No. 1.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C499D449A585F8A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                       229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .4e-50
                                                                                                                                                                                                       ĄĄ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
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5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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SOOC A REPERENCE OF SOCIAL PROPERTIES AND SOCIAL PROPERTIES OF SOCIAL PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T., Turka L.A., Mao X., Nunez G., Thompson C.B.; "bcl-x, a bcl-2-related gene that functions as a dominant regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of apoptotic cell death.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (SHORT FORM). MEDLINE=93364977; PubMed=8358789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              spermatogenesis.";
Mol. Reprod. Dev.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vilagrasa X., Mezquita C., Mezquita J.; "Differential expression of bcl-2 and bcl-x during chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (LONG FORM).
STRAIN-HUBBARD WHITE MOUNTAIN; TISSUE-Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97264485; PubMed=9110311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; 223110; CAA80657.1;
EMBL; U26645; AAB07677.1;
PIR; A47537; A47537.
HSSP; P53563; 1AF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified
                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00452; Bcl-2; Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003093; BH4.
InterPro; IPR000712; Bcl_2.
          SEQUENCE
                                                         VARSPLIC
                                                                                   TRANSMEM
                                                                                                           DOMAIN
                                                                                                                                                       DOMAIN
                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                         Apoptosis;
                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nterPro; IPR002475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-
APOPTOTIC ACTIVITY (BY SIMILARITY).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).

SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74:597-608(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and this statement is not removed.
                                                                                                                                                                                                                                                        PS01259;
PS01260;
                                                                                                                                                                                                                                   PS50063;
                                                                                                                                                                                                                                                                                                       PS01080; BH1;
PS01258; BH2;
                                                                                                                                                                                                                                                                                                                                                      PS50062;
                                                                                                                                                                                                           Transmembrane;
             229 AA;
                                                                                                                                                                                                                                   BH4_1; 1.
BH4_2; 1.
                                                                                                                                                                                                                                                                                       BH3;
                                                                                                                                                                                                                                                                                                                                                      BCL2_FAMILY;
                                                                   144
191
223
229
               25733 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BCL2_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ۲.
                                                                                                                                                                                                                 Alternative
POTENTIAL.

ERFVDLYGNNAAAELRKGQETFNKWLLTGATVAGVLLLGSL
LSRK -> VRTALP (IN SHORT ISOFORM).

; A97D3A4D04C0E9DA CRC64;
                                                                                                                BH2
                                                                                                                                                                                                                 splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bу
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                -I- DOMAIN: The BH4 domain is required for anti-apoptotic activity. The BH1 and BH2 domains are required for both heterodimerization with other Bcl2 family members and for repression of cell death. Forther proteolytically cleaved by caspases during apoptosis (By similarity). The cleaved protein, lacking the BH4 domain, has properly cactivity (By similarity).

-I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-I- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
-I- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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EMBL; AJ001203; CAA04597.1; -. HSSP; Q07817; 1MAZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   myocardium of pig.";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Expression of apoptosis-associated genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bartling B., Hoffmann J., Holtz J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apoptosis regulator Bcl-x. BCL2L1 OR BLC2L OR BCLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  077737;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BCLX_PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 EFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 RFVDLYGNNA----AAELRKGQETFNKWLLTGATVAGVLL-LGSLLSRK 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   caspases (By similarity). Appears to regulate cell death by blocking the volatage-dependent anion channel (VDAC) by binding to it and preventing the release of the caspase activator, cytochrome c, from the mitochondrial membrane. SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By similarity). Heterodimerization with BAX does not seem to be required for anti-apoptotic activity (By similarity). SUBCELULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR DOMAIN: The DUAL Accessor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 LFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWWVAYLETRLADWIHSSGGWA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 VHRSSLEVHEIVRASDVRQALRDAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38 -----AADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQVSDE 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  u
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RELVIDFVSYKLSQRGHCWSELEEEDENRTDTAAEAEMDSVLNGSPSWHPPAGHVVNGAT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.6%; Score 429.5; DB 1
41.2%; Pred. No. 3.3e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schulz R., Heusch G., Dan
genes in hibernating and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Darmer D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     stunned
                                                                                                                                                                                                                                                                                           has pro-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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BCIX_MOUSE STANDARD:

ID BCIX_MOUSE STANDARD:

AC Q64373; Q60657; Q60658; Q61338;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
TISSUE=Pre-B cell;
    SEQUENCE FROM N.A. (ISOFORMS X(L); X(S) AND X(DELTA-TM))
                                    development and its product localizes Development 120:3033-3042(1994).
                                                                                         Gonzalez-Garcia M., Perez-Ballestero R., Ding L., Duan L., Boise L.H.,
                                                                                                              STRAIN=C57BL/6; TISSUE=Brain; MEDLINE=95331139; PubMed=7607090;
                                                                                                                                                                   Kamesaki H., Michaud G.Y., Takatsu K., Okuma M.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                     STRAIN-2A4B;
                                                                                                                                                                                                                                                                                                      Apoptosis regulator Bcl-x. BCL2L1 OR BCL2L OR BCLX.
                                                                "bcl-XL is the major bcl-x mRNA form expressed during
                                                                                    Thompson C
                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA))
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002475; BCL2_family.
InterPro; IPR003093; BH4.
InterPro; IPR000712; Bcl_2.
Pfam; PF00452; Bcl_2; 1.
Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS01258; PROSITE; PS01259; PROSITE; PS01260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 NGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTLAGVVLLGSL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00337; BCL; 1
SMART; SM00265; BH4; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 QVLNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50062; BCL2_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 RALVADFVGYRLRQKGY-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 RELVVDFLSYKLSQKGYSWSQFTDVEENRTEAPEGTESEAETPSAINGNPSWHLADSPAV 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS01260; BH4_1; 1.
PS50063; BH4_2; 1.
                                                                                 .B., Nunez G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS01080;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210
233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitochondrion; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      вн2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.5%; Score 428.5; DB 1; 41.3%; Pred. No. 4.1e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26061 MW; 18BF6FA0441912B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BH1.
                                                    to mitochondria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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use by non-profit institute. There are no restricted and this statement is not removed. Usage her or send an amount a license advanced to send an amount of the send and the send
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Ohta S., Seldin M.F., Nunez G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6 X CBA; TISSUE=Thymus; MEDLINE=98051053; PubMed=9390687; Yang X F., Weber G.F., Cantor H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         apoptosis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fang W., Rivard J.J., Mueller D.L., Behrens T.W.; "Cloning and molecular characterization of mouse bcl-x in
                            EMBL;
EMBL;
EMBL;
HSSP;
                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97289584; PubMed=9144489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunity 7:629-639(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM X(BETA)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95052604; PubMed=7963517;
Fang W., Rivard J.J., Mueller D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lymphocytes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genomic organization, promoter region analysis, localization of the mouse bcl-x gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         novel Bcl-x isoform connected to the
pptosis in T cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               with other Bcl2 family members and for repression of cell pyms: Proteolytically cleaved by caspases during apoptosis similarity). The cleaved protein, lacking the BH4 domain, apoptotic activity (By similarity).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    isoform promotes apoptosis.

SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By similarity). Heterodimerization with BAX does not seem to be similarity). Heterodimerization with BAX does not seem to be required for anti-apoptotic activity (By similarity) required for anti-apoptotic activity (By similarity) SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBERAND PERINUCLEAR SUBELLULAR LOCATION: MITOCHONDRIAL MEMBERAND PERINUCLEAR ENVELOPE FOR BCL-X(L).

SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBERAND PERINUCLEAR SUBCLEDE FOR BCL-X(L).

ALTERNATIVE PRODUCTS: 4 ISOFORMS: BCX-X(L) (SHOWN HERE), BLL-X(S), ALTERNATIVE PRODUCTS: 4 ISOFORMS: BCX-X(L) (SHOWN HERE), BLL-X(S),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN: The BH4 domain is required for The BH1 and BH2 domains are required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEVELOPMENTAL STAGE: BCL-X(BETA)IS EXPRESSED IN BOTH EMBRYONAL AND POSTNATAL TISSUES, WHEREAS BCL-X(L) IS PREDOMINANTLY FOUND IN POSTNATAL TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to it and preventing the release of the caspase cytochrome c, from the mitochondrial membrane. T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   caspases (By similarity). Appears to regulate cell death by blocking the volatage-dependent anion channnel (VDAC) by binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Potent inhibitor of cell death.
                                           X83574; CAA58557.1;

L35049; AAA51039.1;

L35049; AAA51040.1;

U10102; AAA82174.1;

U10102; AAA82174.1;

U10100; AAA82173.1;

U10100; AAA82172.1;

U10100; AAC53460.1;

U78031; AAB96881.1;

U78030; AAB96881.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BCL-X(BETA) AND BCL-X(DELTA-TM); ARE PRODUCED BY ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS\text{-PROT} entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
  MGI:88139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IN, THYMUS, BONE MARROW, AND KIDNEY.
EXPRESSION IS ENHANCED IN B AND T L'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIFICITY: WIDELY EXPRESSED, WITH HIGHEST LEVELS IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158:4750-4757(1997).
  Bc121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domain is required for anti-apoptotic activity
                                                                                      . . . . . . . . . . . . . . . .
                                                         JOINED.
                                                                                                                                                                                                                                                                                                                                                      moved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T cell receptor regulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T LYMPHOCYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for both heterodimerization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BCL-X(L)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Bcl-x(S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND BCL-X(DELTA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                             restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THAT HAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                activation
                                                                                                                                                                                                                                                                                                                                                                                         and
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                                                                                                                                                                                                                                                                                                                                                                                         for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       z
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 Query Match
Best Local S
Matches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00452; Bc1-2; 1.
Pfam; PF02180; BH4; 1.
SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
PR0SITE; PS01062; BC12_F
PROSITE; PS01080; BH1; 1.
PR0SITE; PS01258; BH2; 1.
                                                                                                                                                                                 P53563; Q62678; P70614; P70613; Q62836; Q64087; Q1-QCT-1996 (Rel. 34, Created) Q1-NQV-1997 (Rel. 35, Last sequence update) 16-QCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apoptosis; Mitochondrion; DOMAIN 4 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003093; BH4.
InterPro; IPR000712; Bcl_2.
                                                                                                                                                           Apoptosis regulator Bcl-x. BCL2L1 OR BLC2L OR BCLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
 Submitted
                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                              BCLX_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC
         Wesselingh S.L.,
                      TISSUE-Brain;
                                 SEQUENCE FROM N.A.
                                                       Submitted
                                                                  Michaelidis
                                                                              TISSUE=Brain;
                                                                                         SEQUENCE FROM N.A.
                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                        185
                                                                                                                                                                                                                                                                                                            141
                                                                                                                                                                                                                                                                                                                                   125
                                                                                                                                                                                                                                                                                                                                                         81
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                                                                                                                                                                                                                                                                                                                                                                                                       29
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                                                                                                                                                                                                                                                                                                   SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                              QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAXLETRLADWIHS 140
                                                                                                                                                                                                                                                                                       NGGWDTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL
                                                                                                                                                                                                                                                                                                                                                                                NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE
                                                                                                                                                                                                                                                                                                                                                                                                      CGAGPGEGPAAD------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
                                                                                                                                                                                                                                                                                                                                                                                                                             RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV
                                                                                                                                                                                                                                                                                                                                   QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity 40.9
92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P$50063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS01260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS01259;
h S.L., David G.L., (JUN-1995) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR002475; BCL2_family.
                                                       is T.M.;
(DEC-1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86
129
180
180
210
126
189
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                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BH4_1; 1.
BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BCL2_FAMILY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24
100
148
195
226
188
233
                                                                                          (ISOFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.2%;
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                                                       the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 425.5;
Pred. No. 7.5e
?3; Mismatches
 EMBL/GenBank/DDBJ
                                                        EMBL/GenBank/DDBJ
          Choi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
MISSING (IN ISOFORM BCL-X(S)).
DTFVDLYGNNAAAESKKGQERENKWFLTGMTVAGVVLLGSL
FSRK -> VRTTPLVCPPLACVSLLCEHP (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X(DELTA-TM)).
24D2AC79887E072E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSLFSRK -> GHDCGWCGSAGLTLQSEVTRH (IN ISOFORM BCL-
                                                                                          X(L) AND X(S)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BCL-X(BETA))
                                                                                                                                                                                                                                PRT;
                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
          s,
                                                                                                                                                                                                                                233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  splicing; Transmembrane
             Veliuona M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57;
 databases
                                                          databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
             Hardwick J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53;
                                                                                                                             Rattus
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EMBL;
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                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;

"Expression of members of the bcl-2 gene family in the immature rat ovary: equine chorionic gonadotropin-mediated inhibition of granulosa cell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-x.ong messenger ribonucleic acid levels.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shiraiwa N., Inohara N., Okada S., Yuzaki M., Shoji S.-I., Ol
"An additional form of rat Bcl-x, Bcl-xbeta, generated by an
unspliced RNA, promotes apoptosis in promyeloid cells.";
J. Biol. Chem. 271:13258-13265(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [3] SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Crystal structure of rat Bcl-xL. Implications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Morikawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aritomi M., Kunishima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endocrinology 136:232-241(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN: The BH4 domain is required for anti-apoptotic activity. The BH1 and BH2 domains are required for both heterodimerization with other Bcl2 family members and for repression of cell death. PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity (BP similarity).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1). SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2). SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3). SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH4). SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH4). SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol. Chem. 272:27886-27892(1997). - FUNCTION: Potent inhibitor of cell
                    ; X82537; CAA57886.1; ...
; X82537; CAA57887.1; ...
; U10579; AAA17257.1; ...
; U72350; AAB17353.1; ...
; U72349; AAB17352.1; ...
; U34963; AAA77686.1; ...
; S76513; AAC60702.1; ...
; S78284; AAC60702.1; ...
; AAF3; 07-UJL-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OVARY, THE PREDOMINANT FORM IS BCL-X(L), WITH A SMALL BUT DETECTABLE LEVEL OF BCL-X(S).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             caspases (By similarity). Appears to regulate cell death by blocking the volatage dependent anion channnel (VDAC) by binding
                             1AF3;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the Entransaction in the contract of the Swiss Institute of Bioinformatics and the Technology of the Swiss Institute of Bioinformatics and the Entransaction of the Swiss Institute of Bioinformatics and the Swiss Institute of the Swiss Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein family."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tent inhibitor of cell death. Inhibits similarity). Appears to regulate cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ISOFORMS X(L) AND X(S))
BCL2_family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Ovary;
                                                                               ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inohara N., Ishibashi Y., Ohta
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RESULT 8
BCLX_HUMAN
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Best Local
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                                                                                                               BCLX_HUMAN STANDARU
QO7817; Q92976;
Q07817; Q92976;
Q1-FEB-1995 (Rel. 31, C
Q1-FEB-1995 (Rel. 31, L
Q1-MAR-2002 (Rel. 41, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
PROSITE; PS50062; BCL2_FAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01250; BH4—1; 1.
PROSITE; PS01260; BH4—2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
CONFLICT
SEQUENCE
 SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
MEDLINE=93364977; PubMed=8358789;
Boise L.H., Gonzalez-Garcia M., Postema C.E.
Turka L.A., Mao X., Nunez G., Thompson C.B.;
                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                           Apoptosis regulator Bcl-x.
BCL2L1 OR BCL2L OR BCLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
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                                                    NCBI_TaxID=9606;
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InterPro; IPR000712;
                                                                                                                                                                                                            185 NGGWDTFVDLYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229
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                                                                                                                                                                                                                                SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                   QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE
                                                                                                                                                                                                                                                                                           NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE
                                                                                                                                                                                                                                                                                                                CGAGPGEGPAAD------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT
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Conservative
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                                                                                                                                                           STANDARD;
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Bcl_2.
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FSRK -> VRTTPLVCPPLVCLSSVEIPNCPFWSPGMVVED
IDYSGDIPGLL (IN ISOFORM BCL-X(BETA)).
R -> Q (IN REF. 1).
F -> S (IN REF. 2).
A -> E (IN REF. 4).
A -> V (IN REF. 4).
FF -> SS (IN REF. 4).
                                                                                                                          sequence update)
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BH2.
POTENTIAL.
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-> P (IN REF. 4).
2B62B6C63864BC8F CRC64;
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[7]
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          Lindsten T.,
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Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J., Thompson C.B., Fesik S.W.;
"Structure of Bcl-xL-Bak peptide complex: recognition between regulators of apoptosis.";
Science 275:983-986(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98118550; PubMed=9435230;
Clem R.J., Cheng E.H.-Y., Karp C.L., Kirsch D.G.,
Takahashi A., Kastan M.B., Griffin D.E., Earnshaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLEAVAGE BY CASPASES, AND MUTAGENESIS OF MEDLINE=98118550; PubMed=9435230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sattler M., Liang H., Nettesheim D., Meadows R.P., Harlan J. Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J.,
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Cheng E.H.-Y., Levine B., Boise L.H.,
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Yoon H.S., Nettesheim D., Chang B.S., Thompson C.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               x-ray crystallography (2.2 angstroms), and structure medline=96256675; pubMed=8692274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97172562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Modulation of cell death bx Bcl-xL through caspase interaction.";
Proc. Natl. Acad. Sci. U.S.A. 95:554-559(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hardwick J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 381:335-341(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 379:554-556(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Bax-independent inhibition of apoptosis by Bcl-XL.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Korsmeyer S.J.;
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activity.
SIMILARITY:
SIMILARITY:
                                                                                                                                                                                     ENVELOPE (BY SIMILARITY).

ALTERNATIVE PRODUCTS: 3 ISOFORMS; BCL-X(L) (SHOWN HERE), BCL-X(S) ALTERNATIVE PRODUCED BY ALTERNATIVE SPLICING.

AND BCL-X(BETA), ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: BCL-X(S) IS EXPRESSED AT HIGH LEVELS IN CELLS THAT UNDERGO A HIGH RATE OF TURNOVER, SUCH AS DEVELOPING LAWPHOCYTES. IN CONTRAST, BCL-X(L) IS FOUND IN TISSUES CONTAINING LONG-LIVED POSTMITOTIC CELLS, SUCH AS ADULT BRAIN.

DOMAIN: The BH4 domain is required for anti-apoptotic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Potent inhibitor of cell death. Inhibits activation of caspases (By similarity). Appears to regulate cell death by blocking the volatage-dependent anion channnel (VDAC) by binding to it and preventing the release of the caspase activator, cytochrome c, from the mitochondrial membrane. The Bcl-x(S)
                                                                                                                                                                                                                                                                                                                                                                                                                            apoptotic activity.
SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isoform promotes apoptosis.
SUBUNIT: Bcl-x(L) forms het
                                                                                                                The BH1 and BH2 domains are required for both heterodimerization with other Bc12 family members and for repression of cell death. PTM: Proteolytically cleaved by caspases during apoptosis. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: Bcl-x(L) forms heterodimers with Heterodimerization with BAX does not seem
                                                                                   cleaved protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Natl. Acad. Sci.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ohta
     CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=9020082;
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                                                                                      lacking the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U.S.A. 92:7834-7838(1995)
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     \mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human Bcl-xL, an inhibitor of
                                                                                by caspases dura
BH4 domain, has
     HOMOLOGY DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kirsch D.G., Ueno K.,
Earnshaw W.C., Veliuona M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thompson C.B., Hardwick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASP-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boise L.H., Thompson C.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BAX, B
  1 (BH1).
1 2 (BH2).
                                                                                      pro-apoptotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BAK and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harlan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BAK and Bcl-2
required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wong
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CONFLICT
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                                                                                                                                                                                                                                                                                                                              VARSPLIC VARSPLIC
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                                                                                                                                                                             MUTAGEN
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                    SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50062; BCL2_FAMILY; PROSITE; PS01080; BH1; 1. PROSITE; PS01258; BH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00452; Bcl-2; Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U72398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use
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                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                            Apoptosis;
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                                                                                                                                                                                                               MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                               3D-structure.
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1LXL; 21-APR-97
1MAZ; 21-APR-97
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                                                              RALVADFVGYRLRQKGY---
NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE
                    CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Z23116; CAA80662.1;
Z23115; CAA80661.1;
U72398; AAB17354.1;
                                         RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SM00337; BCL; 1.
SM00265; BH4; 1.
                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      PS01260; BH4_1; 1. PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR003093;
IPR000712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ean Bioinformatics Institute. There are no rest non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS01259; BH3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR002475;
                                                                                                                                                                                                                                                                                                                                                                                                                             Mitochondrion;
                                                                                                                                     233 AA;
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129
180
210
210
126
189
                                                                                   Conservative
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156
176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                              138
148
156
176
189
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137
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100
148
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226
61
188
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70
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                                                                                                                                      26049 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bcl_2.
                                                                                             42.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . . . .
                                                                                                                                                                                                                                                                                                                                                                                                                            Alternative splicing; Transmembrane;
                                                                                   23;
                                                                                                                                                                                       ACTIVITY.
G->A: NO |
G->E: NO |
D->A: NO |
D->A: NO |
                                                                                 Score 424.5; DB Pred. No. 9.2e-313; Mismatches 5
                                                                                                                                         BY ABOUT HALF.
D->A: NO EFECT ON CASPASE-1 CLEAVAGE.
G -> A (IN REF. 1; CAA80661).
                                                                                                                                                                                                                                                       VNW->AIL:
ACTIVITY.
                                                                                                                                                                                                                                                                                                                  CLEAVAGE BY CASPASE-1.
MISSING (IN ISOFORM BCL-X(S)).
DTFVELYGNNAAAESRKGQERENRWFLTGMTVAGVVLLGSL
FSRK -> VRTKPLVCPFSLASGQRSFTALLLYLFLLCWVI
                                                                                                                                                                               WD->GA: REDUCES ANTI-APOPTOTIC ACTIVITY
                                                                                                                                                                                                                                             GRI->ELN: LOSS OF ANTI-APOPTOTIC
                                                                                                                                                                                                                                                                           FRD->VRA:
                                                                                                                                                                                                                                                                                       CASPASE-3
                                                                                                                                                                                                                                                                                                          VGDVDS (IN ISOFORM BCL-X(BETA)
                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                      E09D3CDD851AE9BE CRC64;
                                                                                                                                                                                                                                                                                                 NO CLEAVAGE
                                                                                                                                                                                        EFECT ON CASPASE-1 CLEAVAGE.
                                                                                                                                                                                                            HETERODIMERIZATION WITH
                                                                                                                                                                                                                                                                NO HETERODIMERIZATION WITH LOSS OF ANTI-APOPTOTIC
                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                 BY CASPASE-1
                                                                                                      Length
                                                                                   Indels
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                                                                                   Gaps
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Q00709;
01-APR-1993 (Rel. 25, 0
01-APR-1993 (Rel. 25, 1
16-OCT-2001 (Rel. 40, 1
                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning and DNA sequence analysis of cDNA encoding chicker homologue of the Bc1-2 oncoprotein.", Biochim. Biophys. Acta 113:109-113(1992).

-I- FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding t the apoptosis-activating factor (APAF-1).

-I- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and analysis of controlling the controlli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eguchi Y., Ewert D.L., Tsujimoto Y.;
"Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cazals-Hatem D.L., Louie D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=B-cell lymphoma;
MEDLINE=92379084; PubMed=1511008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=92375724; PubMed=1508712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apoptosis regulator Bcl-2.
BCL2 OR BCL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic Acids Res. 20:4187-4192(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               adult and embryo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125
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                                                                                                                                                                                                                                             DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAF-1 (By similarity).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).

SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kidney,
thymus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bcl-x(L). Heterodimerization with BAX requires intact BHI and BH2 domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1 and RAF-1 (By similarity) SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum. TISSUE SPECIFICITY: In adult chicken expressed, in thymus, spleen, kidney, heart, ovary and brain, with the highest levels in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                     thymus. In the embryo, highly levels expressed in all tissues with high levels in the bursa of Fabricius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                    (See http://www.isb-sib.ch/announce/
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                                                                                                                                       restrictions
                                                                                                                                                                    EMBL outstation
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                                                                                                                                                                                    RESULT
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Best Local
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EMBL; D11381; BAA01978.1; J
EMBL; Z11961; CAA78018.1; -
PIR; A37332; A37332.
PIR; S24390; S24390.
HSSP; Q07817; 1MAZ.
                                                                                                                                                   BCL2_BOV
002718;
                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
CONFLICT
SEQUENCE
STRAIN=HOLSTEIN; TISSUE=Thymus; Reyes R.A., Cockerell G.L.; "Bovine leukemia virus associat
                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seg
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                              SEQUENCE FROM N.A.
                                                            Bovidae;
                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                        Bos taurus (Bovine).
                                                NCBI_TaxID=9913;
                                                                                                             Apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000712; Bcl_2.
Pfam; PF00452; Bcl-2; 1.
Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00337; BCL; SMART; SM00265; BH4;
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                                                                                                                                                                                                                                     145
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                                                                                                                                                                                                                 190 DAFVELYGN----SMRPLFDFSWISLKTILS-LVLVGACITLGAYLGHK
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                                                                                                                                                               BOVIN
                                                                                                                                                                                                                                    AEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK
                                                                                                                                                                                                                                                                         ELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGW 144
                                                                                                                                                                                                                                                                                                                                     DNREIVLKYIHYKLSQRGYDWAAGEDRPPVPPAPAPAAAPAAVAAAGASSHHRPEPPGSA
                                                                                                                                                                                                                                                      ELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIATWMTEYLNRHLHNWIQDNGGW
                                                                                                                                                                                                                                                                                              AASEVPPAEGLRPAPPGVHLALRQAGDEFSRRYQRDFAQMSGQLHLTPFTAHGRFVAVVE
                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                            Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS01080;
PS01258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS50063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS01260;
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                                                                                                            regulator
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IPR003093; BH4
                                                                                                                                                                                                                                                                                                                                                                                                                          121
139
233 /
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                               STANDARD;
                                                             Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BH4_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BCL2_FAMILY;
                                                                                                                                                                                                                                                                                                                                                                                                                             121
139
25687
                                                                   Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                              Bc1-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BCL2_family
                                                                                                                        Last annotation
                                                                                                                                Last sequence update;
associated-leukemogenesis is
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Pred. No. 2.1e
33; Mismatches
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G -> V (IN REF. 2).
; 5252555ACB6E4C3D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSAAASEVPPAEGLRP -> ARLLLVRCPRLRGCA
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                                                                                                                                                               PRT;
                                                                                                                                                               229
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permeability, Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (APAF-1) (By similarity).

-: SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1 and RAF-1 (By similarity).

-: SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum (By similarity).

-: DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAF-1 (By similarity).

-: PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle(By similarity). In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases. Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    with suppression of programmed cell death and increased expression of nal-2 ".
                                                                                                                                                                                                                                                                                                                         SMART; SM00337; BCL; SMART; SM00265; BH4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U92434; AAB53319.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
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SEQUENCE
                                                                                                                                   DOMAIN
                                                                                                                                                                                                           PROSITE;
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                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP;
                                                         TRANSMEM
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                                                                                               DOMAIN
                                                                                                                 DOMAIN
                                                                                                                                                     DOMAIN
                                                                                                                                                                                         Apoptosıs;
                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                       PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity).

PTM: Profeolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity (By similarity).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cell. Regulates cell death by controlling the mitochondrial membrane
                                                                                                                                                                                                                                                                                                                                                             PF00452; Bcl-2; 1. PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q07817;
                                                                                                                                                                                                             PS50063;
                                                                                                           ; Transmembrane; N
10 30
64 68
69 72
83 97
                                                                                                                                                                                                                                                                                                                                                                                               IPR002475; BCL2_family.
IPR003093; BH4.
IPR000712; Bc1_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1MAZ
                                                                                                                                                                                                           BH4_1; 1.
BH4_2; 1.
                                                                                                                                                                                                                                                                   вн2;
                                                                                                                                                                                                                                                 внз;
                                                                                                                                                                                                                                                                                     BCL2_FAMILY;
BH1; 1.
   25099
                                                                                                                                                                                         Mitochondrion; Phosphorylation
   ž
                                                                                                           POLY-PRO.
POLY-ALA.
BH3.
BH2.
POTENTIAL.
CLEAVAGE (BY CASPASES) (BY SIMILARITY).
PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
ADIDDOAF98FFF11D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (See http://www.isb-sib.ch/announce/
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RESULT
BCL2_RA
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P49950; Q628
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-SPRAGUE-DAWLEY; TISSUE-Ovary; MEDLINE-95129487; pubMed=7828536; MEDLINE-95129487; pubMed=7828536; Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.; Expression of members of the bcl-2 gene family in the immature recovery: equine chorionic gonadotropin-mediated inhibition of granucell apoptosis is associated with decreased bax and constitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels."; Endocrinology 136:232-241(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Apoptosis regulator Bcl-2.
BCL2 OR BCL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996 (Rel. 34, Created)
01-NOV-1997 (Rel. 35, Last sequence ul)
16-OCT-2001 (Rel. 40, Last annotation
 -
                                                                                                                                                                                                                                                                                                                       Castren E., Ohga Y.,
                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 19-172 FROM N.A. MEDLINE=95059917; PubMed=7969891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning and sequencing of a cDNA encoding the rat Bc1-2 protein."; Gene 140:291-292(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94193015; PubMed=8144041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                   adult rat brain.";
Neuroscience 61:165-177(1994).
                                                                                                                                                                                                                                                                                   "bcl-2 messenger RNA is localized in neurons of
                                                                                                                                                                                                                                                                                                         Lindholm D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
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                                                                                                  FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (APAF-1).

SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and solutions in the control of the substantial statements.
                              domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1 and RAF-1 (By similarity) SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
                                                                                      Bcl-x(L). Heterodimerization with BAX requires intact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAGPAPSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARERFATVVEELFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T., Irie S., Krajewski S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGVNWGRIVAFFEFGGVMCVESVNREMSPLVDSIALWMTEYLNRHLHTWIQDNGGWDAFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85
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SPECIFICITY: Expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
of the nuclear envelope and the endoplasmic reticulum PECIFICITY: Expressed in a variety of tissues, with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q64032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                        Berzaghi M.P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 412.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reed J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NO.
                                                                                                                                                                                                                                                                                                                          Tzimagiorgis G., Thoenen H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236
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                                                                                            BH1
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                                                                                          and BH2
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B
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CONFLICT
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-i- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle. In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases. By similarity). Dephosphorylated by protein phosphorylated by protein phosphorylated protein cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity (By similarity).
-i- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-i- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-i- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
-i- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                      SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a clotween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for
                                                                                                                                                                                                                      SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                 SEQUENCE
                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                       MOD_RES
                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                     PROSITE; PS01260; PROSITE; PS50063;
                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50062;
                                                                                                                                                                                                                                                                                                                                                                                                           SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP;
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                                                                                                                                                                                                                                                                                                         Apoptosis;
                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
  10
                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                  erPro; IPR002475; BCL2_fa

srPro; IPR003093; BH4_

srPro; IPR000712; Bel_2.

srPro; IPR000712; Bcl_2;

srPr00452; Bcl_2; 1.

srPr00452; Bcl_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                highest levels in reproductive tissues. In the adult brain, expression is localized in mitral cells of the olfactory bulb, granule and pyramidal neurons of hippocampus, pontine nuclei, cerebellar granule neurons, and in ependymal cells. In prenatal brain, expression is higher and localized in the neuroepithelium and in the corrical plate.
DNREIVMKYIHYKLSQRGYEWDTGDEDSAPLRAAPTPGIFSFQPESNRTPAVHRDTAART
                             DTRALVADFVGYRLRQKGY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U34964;
S74122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q07817; 1MAZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L14680; AAA53662.1; -. U34964; AAA77687.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                          SM00337; BCL;
SM00265; BH4;
                                                                       Similarity
                                                                                                                                                                                                                                                                                                                     PS01258; BH2; 1.
PS01259; BH3; 1.
PS01260; BH4_1;
PS50063; BH4_2;
                                                                                                                                                                                                                                                                                                                                                                              PS01080; BH1;
                                                                                                                                                                                                                                                                                                        Transmembrane;
                                                                                                                                                          10
90
133
184
209
209
34
70
70
157
                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                           BCL2_FAMILY;
                                                                                                                                                          30
104
152
199
230
230
35
70
42
157
                                                                                                                                 26622 MW;
                                                                       40.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BCL2_family.
                                                                                                                                    BH2.

POTENTIAL.

CLEAVAGE (BY CASPASES) (BY SIMILARITY).

PHOSPHORYLATION (BY PKC) (BY SIMILARITY).

A -> R (IN REF. 2).

E -> G (IN REF. 2).

L -> Q (IN REF. 2).

L -> Q (IN REF. 2).
                                                                                                                                                                                                                                                                                                      Mitochondrion; Phosphorylation
                                                           35;
                                                             Score 410; Up ...
No. 1.8e-29;
62
                                                                                                                                E7688CB9071A872A CRC64;
                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
                                                                                    Length 236;
                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and for
                                                                                                                                                                                                     SIMILARITY).
                                                        52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 collaboration
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BCL2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ρy
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P10417; P10418;
01-MAR-1989 (Rel. 10, C
01-APR-1993 (Rel. 25, I
01-MAR-2002 (Rel. 41, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deng X., Ito T., Carr B., Mumby M., May W.S. Jr.;
"Reversible phosphorylation of Bcl2 following interleukin 3 bryostatin 1 is mediated by direct interaction with protein phosphatase 2A*.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97277291; PubMed=9115213; Ito T., Deng X., Carr B., May W.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic Acids Res. 20:4187-4192(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REVISIONS TO 221-222
MEDLINE=92375724; Pul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Negrini M., Silini E., Kozak C., Tsujimoto Y., Croce C.M.; "Molecular analysis of mbcl-2: structure and expression of the murine gene homologous to the human gene involved in follicular lymphoma."; Cell 49:455-463(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=BALB/C; TIS
MEDLINE=87187643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apoptosis regulator BCL2 OR BCL-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEPHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Bcl-2 phosphorylation required for anti-apoptosis function. J. Biol. Chem. 272:11671-11673(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eguchi Y., Ewert D.L., Tsujimoto Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHORYLATION BY PKC, AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                               nosphatase 2A*..;
Biol. Chem. 273:34157-34163(1998).

Biol. Chem. 273:34157-34163(1998).

FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cycochrome c from the mitochondria and/or by binding the release of cycochrome c from the mitochondria and/or by binding the release of cycochrome c from the mitochondria and/or by binding the release of cycochrome c from the mitochondria and/or by binding the release of cycochrome c from the mitochondria and/or by binding the release of cycochrome c from the mitochondria and/or by binding the release of cycochrome c from the mitochondria and/or by binding the release of cycochrome c from the mitochondria and/or by binding the release of cycochrome c from the mitochondria and/or by binding the release of cycochrome c from the mitochondria and/or by binding the release of cycochrome c from the mitochondria and/or by binding the release of cycochrome c from the mitochondria and/or by binding the release of cycochrome c from the mitochondria and/or by binding the release of cycochrome c from the mitochondria and/or by binding the release of cycochrome c from the mitochondria and/or by binding the release of cycochrome c from the mitochondria and/or by binding the release of cycochrome c from the mitochondria and/or by binding the release of cycochrome c from the mitochondria and/or by binding the release of cycochrome c from the mitochondria and/or by binding the release of cycochrome c from the mitochondria and/or by binding the release of cycochrome c from the mitochondria and/or by binding the release of cycochrome c from the mitochondria and/or by binding the release of cycochrome controlled the mitochondria and/or by binding the release of cycochrome controlled the mitochondria and/or by binding the re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Isolation and characterization of the chicken in a variety of tissues including lymphoid and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA)
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                                                                                                     Bcl-x(L). Heterodimerization with BAX requires intact domains, and is necessary for anti-apoptotic activity similarity). Also interacts with APAF-1 and RAF-1. SUBCELLULAR LOCATION: Outer mitochondrial membrane, in membrane of the nuclear envelope and the endoplasmic r
are produced by alternative splicing.
TISSUE SPECIFICITY: Expressed in a variety of tissues
DOMAIN: The BH4 domain is required for anti-apoptotic
                                                                            membrane of the nuclear envelope and the endoplasmic ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGWDAFVELYG----PSMRPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . Jr.;
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  anti-apoptotic
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neuronal organs in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bc1-2
                                                                                                                                                                                                                                                                                         and/or by binding to
                                                                                                                                     intracellular
                                                                               reticulum and beta;
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     activity
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cc -i- pTM: phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
cc anti-apoptotic activity. Growth factor-stimulated phosphorylation
cc on Ser-70 by PKC is required for the anti-apoptosis activity and
cc occurs during the G2/M phase of the cell cycle. In the absence of
cc growth factors, Bcl2 appears to be phosphorylated by other protein
cc kinases such as ERKs and stress-activated kinases.
cc pTM: proteolytically cleaved by caspases during apoptosis. The
cc cleaved protein, lacking the BH4 domain, has pro-apoptotic
cc activity, causes the release of cytochrome c into the cytosol
cr similarity: contains 1 Bcl-2 Homology Domain 2 (BH2).
c-i- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH3).
c-i- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
c-i- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
c-i- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
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                                                                                                           Matches
                                                                                                                        Query Match
Best Local
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PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01250; BH4 1; 1.
PROSITE; PS50063; BH4—2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50062;
                                                                                                                                                                                                                                                                                                                                                                                                                          SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L31532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute.
                                                                                                                                                                                                                                  SITE
                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                PhosphoryLation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
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 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A25960; TVMSA1.
B25960; TVMSB1.
E37332; E37332.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGI:88138; Bcl2.
                                                                                DTRALVADFVGYRLRQKGYVCGAG--
SPLRPLVATAGPALSPVPPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129
                           -----EGPAADP----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ
                                                      DNREIVMKYIHYKLSQRGYEWDAGDADAAPLGAAPTPGIFSFQPESNPMPAVHREMAART
                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00452; Bcl-2;
PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM00337; BCL;
SM00265; BH4;
                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR003093; BH4.
IPR000712; Bcl_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR002475; BCL2_family.
                                                                                                                                                                                                                                                                                                                              Alternative
                                                                                                                                                                             236
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90
133
184
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                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          BCL2_FAMILY;
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152
199
230
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70
                                                                                                                                                                             26425 MW;
                                                                                                                        40.5%;
37.1%;
                                                                                                                                                                                                                                                                                                                             splicing; Transmembrane; Mitochondrion;
                                                                                                           35;
                                                                                                                        Score 409; DB 1;
Pred. No. 2.2e-29;
                                                                                                                                                                            POTENTIAL.
CLEAVAGE (BY CASPASES) (BY SIMILARITY).
PHOSPHORYLATION (BY PKC).
PHOSPHORYLATION (BY PKC).
DAFYCLYGPSWRPLFDPSWLSLKTLLSLALVGACITLGAYL
GHK -> VGACLIVE (IN ISOFORM BETA).
AA85EF6B0766BE0A CRC64;
                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       There are no restrictions ong as its content is in
                                                                                   -PG--
                                                                                                                                     DB 1;
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                                                                                                                                    Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           γď
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                                                                                                              52;
                                                                                                             Gaps
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BCL2_HUMAN STANDARD; PRT; 239 AA
BCL2_HUMAN STANDARD;
P10415; P10416; Q16197; Q13842;
O1-MAR-1989 (Rel. 10, Created)
O1-APR-1993 (Rel. 25, Last sequence update)
O1-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-BOLDERY OF THE PROPERTY M.L., Smith S.D., Sklar J.; Cleary M.L., Smith S.D., Sklar J.; "Cloning and structural analysis of cDNAs for bcl-2 and "Cloning and structural analysis of cDNAs for bcl-2 and "Cloning and structural analysis of cDNAs for bcl-2 and "Cloning and structural analysis of cDNAs for bcl-2 and "Cloning and structural analysis of cDNAs for bcl-2 and "Cloning and structural analysis of cDNAs for bcl-2 and "Cloning and structural analysis of cDNAs for bcl-2 and "Cloning and structural analysis of cDNAs for bcl-2 and "Cloning and structural analysis of cDNAs for bcl-2 and "Cloning and structural analysis of cDNAs for bcl-2 and "Cloning and structural analysis of cDNAs for bcl-2 and "Cloning and structural analysis of cDNAs for bcl-2 and "Cloning and structural analysis of cDNAs for bcl-2 and "Cloning analysis" and "Cloning analysis" analysis of cDNAs for bcl-2 and "Cloning analysis" and "Cloning analysis" analysis of cDNAs for bcl-2 analysis of cDNA
                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92096610; PubMed=1339299;
Tanaka S., Louie D.C., Kant J.A., Reed J.C.;
"Prequent incidence of somatic mutations in translocated BCL2
oncogenes of non-Hodgkin's lymphomas.";
Blood 79:229-237(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Alternative promoters and exons, somatic mutation of the Bcl-2-Ig fusion gene in lymphoma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM ALPHA).
MEDLINE=88196071; PubMed=2834197;
Seto M., Jaeger U., Hockett R.D., Graninger W., Bennett S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eguchi Y., Ewert D.L., Tsujimoto Y., respectively. Tsolation and characterization of the chicken bcl-2 gene: expression \Gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REVISIONS TO 96; 110 AND 237.
MEDLINE=92375724; Pubmed=1508712;
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"Analysis of the structure, transcripts, and protein products bcl-2, the gene involved in human follicular lymphoma.";
proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apoptosis regulator Bcl-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goldman P., Korsmeyer S.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell 47:19-28(1986).
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apoptosis
   Yin X.-M., Oltvai 2.N., Korsmeyer S.J.;
"BH1 and BH2 domains of Bcl-2 are required for inhibition
apoptosis and heterodimerization with Bax.";
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                                                                                     MEDLINE=94239528; PubMed=8183370;
                                                                                                                           MUTAGENESIS
                                                                                                                                                                                                         programmed
                                                                                                                                                                                                                                                                  Hockenbery D., Nunez
                                                                                                                                                                                                                                                                         MEDLINE=91066924; PubMed=2250705; Hockenbery D., Nunez G., Milliman C.,
                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-131 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                variety of tissues including lymphoid and neuronal organs
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                                                                                                                                                                                                                is an inner mitochondrial mmed cell death.";
                                                                                                                                                                             nmed cell death.";
348:334-336(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ISOFORM ALPHA), AND VARIANTS NHL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                            membrane protein that
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                                                                                                                                                                                                                                                                         Schreiber R.D., Korsmeyer S.J.;
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use by non-profit institutions as rung use by and for commercan modified and this statement is not removed. Usage by and for commercan modified and this statement is not removed. Usage by and for commercant modified and this statement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                -!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
-!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).
-!- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
-!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                    the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1 and RAF-1.
-!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum.
-!- ALTERNATIVE PRODUCTS: 2 isoforms; alpha (shown here) and beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamamoto K., Ichijo H., Korsmeyer S.J.;
"BCL-2 is phosphorylated and inactivated by an ASK1/Jun N-terminal protein kinase pathway normally activated at G(2)/M.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruvolo P.P., Deng X., May W.S.;
"Phosphorylation of Bcl2 and regulation of apoptosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20036804;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Conversion of Bcl-2 to a Bax-like death effector by caspases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLEAVAGE BY CASPASES, AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                      promoting further caspase activity.

DISEASE: Involved in follicular lymphoma (FL) (also known as type II chronic lymphatic leukemia) by a chromosomal translocation t(14;18)(q32;q21) which involves Bcl2 and immunoglobulin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle. In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as EKS and stress-activated kinases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity). PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               are produced by alternative splicing.
TISSUE SPECIFICITY: Expressed in a variety of tissues.
DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAF-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell. Biol. 19:8469-8478[1999].

FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoletic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the apoptosis-activating factor (APAF-1). SUBUNIT: Forms homodimers, and heterodimers with BAX, Bcl-x(L). Heterodimerization with BAX requires intact
                                                                                                                                                                                                                                                                                                                                                                                                                        regions
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tent is in
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BH1
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EMBL; M13994; AAA51813.1; Z EMBL; M13995; AAA51814.1; Z EMBL; M14745; AAA35591.1; Z EMBL; X06487; CAA29778.1; Z EMBL; S72602; AAD14111.1; Z

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InterPro; IPRO00712; B
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CONFLICT
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PIR; B29409;
PIR; A24428;
PIR; C37332;
PIR; D37332;
                                                                                                                                                                                                                                   SEQUENCE
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VARSPLIC
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190 QDNGGWDAFVELYG----PSMRPLFDFSWLSLKTLLSLAL-VGACITLGAYLGHK 239
                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                    MUTAGEN
                                                                                                                                                                                                                                                                                                                       MUTAGEN
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DOMAIN
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SMART; SM00265; BH4; 1
PROSITE; PS50062; BCL2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proto-oncogene; Apoptosis; Alternative splicing; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00452; Bc1-2; Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; Q07817;
MIM; 151430; -
                                                                                        70
                                                                                                                                  10
                                                                                                                                                    HSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                        FTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWWVAYLETRLADWI 138
                                                                                    SPLQTPAAPGAAAGPALSPVPPVVHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARGR
                                                                                                                               DNREIVMKYIHYKLSQRGYEWDAGDVGAAPPGAAPAPGIFSSQPGHTPHPAASRDPVART 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A29409; TVHUA1.
B29409; TVHUB1.
                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS50062; BCL2_FAMILY; 1
PS01080; BH1; 1.
PS01258; BH2; 1.
PS01259; BH3; 1.
PS01259; BH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS50063; BH4_2; 1.
                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TVHUBC.
; C37332.
; D37332.
                                                                                                                                                                                                                                                                                                 188
                                                                                                                                                                                                                                                                                                                                                                              93
                                                                                                          -----GPAADP----LHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1MAZ.
                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphorylation; Chromosomal translocation;
                                                                                                                                                                                                                                  129 I
26266 MW;
                                                                                                                                                                                                                                                                                                 188
                                                                                                                                                                                                                                                                                                                      34
64
145
                                                                                                                                                                                    40.5%;
36.6%;
                                                                                                                                                                                                                                                                                                                                                                              93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bcl_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BCL2_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mutation
                                                                                                                                                                                                                                         D->A: ABOLISHES CLEAVAGE BY CASPASE-3.
D->A: NO EFFECT ON CLEAVAGE BY CASPASE-3.
G->A: NO HETERODIMERIZATION WITH BAX AND LOSS OF ANTI-APOPTOTIC ACTIVITY.
W->A: NO HETERODIMERIZATION WITH BAX AND LOSS OF ANTI-APOPTOTIC ACTIVITY.
I-> F (IN REF. 4).
P-> T (IN REF. 4).
P-> C (IN REF. 3).
S-> R (IN REF. 4).
                                                                                                                                                                            35,
                                                                                                                                                                                    Score 408.5; DB pred. No. 2.5e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
DAFVELYGPSMRPLFDFSWLSLKTLLSLALVGACITLGAYL
GHK -> VGASGDVS (IN ISOFORM BETA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
CLEAVAGE (BY CASPASE-3).
                                                                                                                                                                                                                                                                                                                                           /FTId=VAR_000829.
D->A: ABOLISHES C
                                                                                                                                                                                                                                                                                                                                                                  MUTATION
                                                                                                                                                                                                                                  3C49F2B714DC9CCB CRC64;
                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                           I (IN NON-HODGKINS-LYMPHOMA; SOMATIC
                                                                                                                                                                                                                                                                                                                                                                                                          (IN NON-HODGKINS-LYMPHOMA; SOMATIC
                                                                                                                                                                                                                                                                                                                                                                                       _000828
                                                                                                                                                                                               ۲.
                                                                                                                                                                                               Length
                                                                                                                                                                          Indels
                                                                                                                                                                          55;
                                                                                                                                                                        Gaps
                                                                                                                                                                         5.
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RESULT
BCL2_CI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apoptosis regulator BCL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Apoptosis regulator Bcl-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND CLEAVAGE BY CASPASES. MEDLINE-21092839; PubMed-11181062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; 8VLL60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BCL2_CRILO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. Biophys. Res. Commun. 275:899-903(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning and functional analysis of cDNA encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tomicic M.T., Christmann M., Kaina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20431763; PubMed=10973819;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochem. Biophys. Res. Commun. 281:404-408(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tomicic M.T., Kaina B.; "Hamster Bcl-2 protein is cleaved in vitro and in cells by
                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                            -
                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                        PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle (By similarity). In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases (By similarity). Dephosphorylated by protein phosphorylated by similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity). Also interacts with APAF-1 and RAF-1 (By Similarity). SUBCELULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum. DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAF-1 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to the apoptosis activating factor (APAF-1) (By similarity). BAK and SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   caspase-3."
                                                                                                                                                                                                                                                                cleaved protein, lacking the BH4 domain, has pro-apopt activity, causes the release of cytochrome c into the promoting further caspase activity.

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 3 (BH3).

SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 4 (BH4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1 and RAF-1 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
  AJ271720; CAB92245.1;
P53563; 1AF3.
                                                                                                                                                                                                                                                                                                                                                                                                                          Proteolytically cleaved by caspases during apoptosis. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        236
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                                                                                                                                                                                                                                                                                                                                                                                  as pro-apoptotic
c into the cytos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hamster Bcl-2
                                                                                                                                                                                                                                                                                                                                                                                      cytosol
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002475; BC
InterPro; IPR003093; BH
InterPro; IPR00712; Bc
InterPro; IPR00712; Bc
Pfam; PF00452; Bc1-2; 1
Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01260; BH4_1; 1. PROSITE; PS50063; BH4_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50062; BCL2_PROSITE; PS01080; BH1; PROSITE; PS01258; BH2; PROSITE; PS01259; BH3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00337; BCL; SMART; SM00265; BH4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                     _XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
-:- FUNCTION: CONFERS STRONG PROTECTION AGAINST CELL DEATH.
-:- SUBCELLULAR LOCATION: Membrane-bound (Potential).
-:- DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE BRAIN OF MID-METAMORPHOSIC TO POST-METAMORPHOSIC TADPOLES AND ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.
-:- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 1 (BH1).
-:- SIMILARITY: CONTAINS 1 BCL-2 HOMOLOGY DOMAIN 2 (BH2).
                                                                                              "Cloning, characterization and expression of two Xenopus bcl-2-like cell-survival genes.";
Gene 158:171-179(1995)
                                                                                                                                         Cruz-Reyes J., Tata J.R.;
                                                                                                                                                       MEDLINE=95331613; PubMed=7607538;
                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                      Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopos
                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                    Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                Apoptosis regulator R11
                                                                                                                                                                       TISSUE-Head
                                                                                                                                                                                                              NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                          190
                                                                                                                                                                                                                                                                                                                                                                                                                                                     142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 DNREIVMKYIHYKLSQRGYEWDVGDVDAAPLGAAPTPGIFSFQPESNPTPAVHRDMAART 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82
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                                                                                                                                                                                                                                                                                                                                                                                                                         GGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVALGALVTVGAFFASK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPLRPIVATTGPTLSPVPPVVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ
                                                                                                                                                                                                                                                                                                                                                    XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane; Mitochondrion; Phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90
133
184
209
209
70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BCL2_FAMILY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bcl_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BCL2_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.5%;
                                                                                                                                                                                                                                                                                     (XRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 399; DB
Pred. No. 1.7e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLEAVAGE (BY CASPASE-3 AND CASPASE-9).
PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BECADF1EF3337228 CRC64;
                                                                                                                                                                                                                                                                                                                                                         204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Search completed: June 10, 2002, 10:32:13 Job time: 346 sec
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Best Local Similarity
Matches 81; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X82461; CAA57844.1; -.
HSSP; Q07817; 1MAZ.
InterPro; IPR002475; BCL2_family.
InterPro; IPR00399; BH4.
InterPro; IPR00399; BCL_2.
InterPro; IPR000712; BCL_2.
Pfam; PF00452; BCl_2: 1.
Pfam; PF02480; BH4; 1.
SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS50062; BCL2_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                               184 RLLTI-VMLTGVFAL 197
                                                                                                                                          124 VESANKEMTDILPRIYQWMVNYLEHTLQFWMQENGGWEAFVGLYGKNAAAQSRESQERFG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apoptosis; Transmembrane.
                                                                                                                 166 NWASVRTVLTGAVAL 180
                                                                                                                                                                   108 AESVNKEMEPLVGQVQDWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLRE--G 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                           48 AAGDEFETRERRTESDLAAQLHVTPGSAQQRETQVSDELFQGGDNWGRLVAFFVFGAALC 107
                                                                                                                                                                                                                                                                                                               σ
                                                                                                                                                                                                                                                                               SRDLVEKFVSKKLSQ-NEACRKFSNNPNPMPYLMEPSTSERPGEGATQGIVEEEVLQALL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                  101 120 BH1.
152 167 BH2.
181 198 POTENTIAL.
204 AA; 23379 MW; 3BFC6BE6DDA4CAO3 CRC64;
                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                             36.3%; Score 366; DB 1; Length 204;
41.5%; Pred. No. 1.2e-25;
tive 25; Mismatches 63; Indels 26; Gaps
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OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0% Maximum Match 10
                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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Perfect score:
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11:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       562222 seqs, 172994929 residues
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                                                                                                                                                                                                                                                                 SPTREMBL_19:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                               Listing first 45 summaries
           sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
                                                                                                        sp_phage:*
sp_plant:*
                                                                                                                                      sp_organelle:*
                                                                                                                                                       sp_mhc:*
                                                                                                                                                                                                                                 sp_bacteria:*
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                                                                                                                                                                                     sp_invertebrate:*
                                                                                                                                                                                                    sp_human:*
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                                                                                         sp_rodent:*
sp_archeap: *
                                                                            sp_virus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

16	15	14	13	12	11	10	9	æ	7	6	u	4	_	w	ν	1		Result No.
347	368	369.5	371.5	371.5	395	397	399.5	401	401	425.5	428.5	400.0	7	436.5	767	1002		Score
34.4	36.5	36.6	36.8	36.8	39.1	39.3	39.6	39.7	39.7	42.2	42.5		429	43.3	76.0	99.3	1 1 1 1 1	Query Match Length DB
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Query Match

99.3%; Score 1002;

DB 11; Length 193;

45	44	43	42	41	40	9	38	37	36	<u>ა</u>	34	ω	32	ω L	30	29	28	27	26	25	24	23	22	21	20	19	18	17
119	121	121.5	124.5	127.5	129.5	130	136	137.5	137.5	137.5	138.5	141	141.5	142	142	144	145	147.5	148.5	154	157.5	162	163	165.5	175.5	177.5	182	187
11.8	12.0	12.0	12.3	12.6	12.8	12.9	13.5	13.6	13.6	13.6	13.7	14.0	14.0	14.1	14.1	14.3	14.4	14.6	14.7	15.3		16.1			, -	•	18.0	
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078480	Z WOMEN	Q923W6	Q923W5	P97287	Q9Z1P3	Q9DH00	Q9NR76	Q9DGJ5	Q91812	Q9UL32	035425	Q919N3	CATTAGO	Q9UMX3	TAGMED	1NZ060	Q9GMG7	Q9NYG7	Q9N754	Q9JKL3	Q9MZS6	QURLBS	Q967D2	Q9H1R5	Q98U13	Q919N4	Q9WUI5	Q9JK59
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## ALIGNMENTS

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RESULT 1

O88996

O88996

O88996;

DT 01-NOV-1998 (TYEMBLrel. 08, Created)
DT 01-DEC-2001 (TYEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TYEMBLrel. 19, Last annotation update)
DE BCL-W.

OC ENCATYOCL; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Enkaryocl; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
FR SEQUENCE FROM N.A.
RA Hamner S., Skoglosa Y., Lindholm D.;
Pifferential expression of bcl-w and bcl-x messenger RNA in the developing and adult rat nervous system.";
RL Neuroscience 91:673-684(1999).
DR InterPro; IPR002475; Bcl-2; 1.
DR HSSP; O78417; 1MAZ.
DR InterPro; IPR003093; Bd4(1999).
DR InterPro; IPR003093; Bd4.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL-1; 1.
DR SMART; SM00337; BCL-2; 1.
DR SMART; SM003265; BH4; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01080; BH2; 1.
DR PROSITE; PS01080; BH4]; 1.
DR PROSITE; PS01080; BH4]; 1.
DR PROSITE; PS01080; BH4]; 1.
DR PROSITE; PS01080; BH2; 1.
DR PROSITE; PS01080; BH2; 1.
DR PROSITE; PS01080; BH2; 1.
DR PROSITE; PS01080; BH4]; 1.
DR PROSITE; PS01080; BH2; 1.
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Local Similarity

99.0%;

Pred. No. 6.7e-80;

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RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boifelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazaraelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Stoch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
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                                                                                                                             MGD; MGI:108052; Bc1212.
InterPro; IPR002475; BCL2_family.
InterPro; IPR007112; Bc1_2.
InterPro; IPR003093; BH4.
InterPro; IPR003093; BH4; I.
INTERPRO; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
PROSITE; PS50062; BCL2_FAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS50063; BH4_2; 1.
SEQUENCE 178 AA; 19147 MW; E2
                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 409:685-690(2001).
EMBL; AK013244; BAB28740.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; Q07817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-C57BL/6J; TISSUE-EMBRYO; MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
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   E2D4C3F79528E9D7 CRC64;
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                                                                                                                                                                                                                                                                                                    PROSITE; PS50062; BCL2_FAMILY; 1.
PROSITE; PS01080; BH1; 1.
PROSITE; PS01258; BH2; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01260; BH4 1; 1.
PROSITE; PS50063; BH4 2; 1.
PROSITE; PS50063; BH4 2; 1.
SEQUENCE 233 AA; 25986 MW; 12F0F30344D53F93 CRC64;
         186
                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00452; Bcl-2; Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AY005131; AAF88137.1; -. HSSP; P53563; 1AF3.
                                                               126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; vei
Mammalia; Eutheria; Lagomorpha; Leporidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002475; BCL2_family.
InterPro; IPR000712; Bcl_2.
InterPro; IPR003093; BH4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryotolagus cuniculus (Rabbit).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2001 (TrEMBLrel. 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BCL-X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9MYW4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Rabbit Bcl-x."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9мүw4
                                                                                   82 VSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS 141
                                                                                                                               66
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                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                      6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTGPEMETPSAINGNPAWHPADSPAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 FSDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEDLVG 120
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GGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229
                           GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
                                                      VVNELFRDGVNWGRIVAFESFGGALCVESVDKEMEVLVSRIAAWMATYLNDHLEPWIQEN 185
                                                                                                              NGATGHSSSLDAREVIPMTAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ
                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Robertson L., James E.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                               43.3%; Score 436.5; DB 6; 41.5%; Pred. No. 2e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.0%;
96.0%;
                                                                                                                                                                                                                                   23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 767; DB 11
Pred. No. 2e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11; Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryctolagus.
                                                                                                                                                                                                                             57; Indels 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Best Local S
Matches 93
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O35844;
01-JAN-1998 (TrEMBLrel. (
01-JAN-1998 (TrEMBLrel. (
01-DEC-2001 (TrEMBLrel. 1
                                                                                  Q9N1A2
Q9N1A2;
Q9N1A2;
01-OCT-2000 (TrE
01-OCT-2000 (TrE
01-DEC-2001 (TrE
ANTI-APOPTOTIC F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A novel Bc1-x isoform connected apoptosis in T cells,"; Immunity 7:629-639(1997).
EMBL; U51278; AAC53459.1; --
HSSP; P53563; 1AF3.
    Eukaryota;
Mammalia;
                                               Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00337; BCL; 1.
SMART; SM00265; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98051053; PubMed=9390687;
Yang X.-F., Weber G.F., Cantor H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-B6/CBA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                          185
                                                                                                                                                                                                                                                                                                                                                  141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ); MGI:88139; BC121.
:errpro; IPR002475; BCL2_family.
:errpro; IPR000712; BCL_2.
:errpro; IPR003093; BH4.
:m; PF00452; BC1-2; 1.
im; PF00180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                               QVSDELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RALVADFVGYRLRQKGY-----
                                                                                                                                                                                                                                                                                                                                                SGGWAEFTALYGDGALEEARRLREG - - NWASYRTYLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                                                          QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIASWMATYLNDHLEPWIQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV
                                                                                                                                                                                                                                                                                                       NGGWDTFVDLYGNNAAAESRKGKEGFNRWFLTGMTVAGVVLLGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS50062; BCL2_FAM:
PS01080; BH1; 1.
PS01258; BH2; 1.
PS01259; BH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS01260;
PS50063;
  ; Metazoa;
Eutheria;
                                                                                                         0 (TrEMBLrel. 15,
0 (TrEMBLrel. 15,
1 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=THYMUS
                                                                                         REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; BH4_1; 1.
; BH4_2; 1.
A; 26033 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BCL2_FAMILY;
BH1; 1.
Chordata; Craniata; Veri
Cetartiodactyla; Suina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.9%;
41.3%;
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19,
                                                                                         BCL-XL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23;
                                                                                                         Last sequence update)
Last annotation updat
                                                                                                                                                      Created)
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 4.4e-30;
                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3083F2D8327E072E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                233
  Vertebrata;
ina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T cell receptor
                                                                                                                                                                                                A
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                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
    Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regulates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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7 99M257
7 99M257
1 D 29
1 D 2
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Best Local
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                                                                                                                                                                                                                                                                                                                                                    Q9MZS7;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
Q1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Q1-OCT-2001 (TrEMBLrel. 18, Last annotation update)
BCL-X LONG PROTEIN.
Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
MCBL_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
PROSITE;
PROSITE;
SEQUENCE
                                                                                                                                                   TISSUE-OVARY;

Murray J.F., Dong Y.B., Leigh A.J., Scaramuzzi
"Bcl-x in the sheep ovary.";

Submitted (JUL-1999) to the EMBL/GenBank/DDBJ
EMBL; AF164517; AAF89532.1;

HSSP; P53563; 1AF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PROSITE;
                  InterPro; IPR003093; BH4. Pfam; PF00452; Bc1-2; 1. Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9MZS7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lee T.L., Canty J.M.;
"PCR Cloning of a Porcine bcl-xL cDNA from Heart.";
"PCR Cloning of a Porcine bcl-xL cDNA from Heart.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF216205; AAF33212.1; ...
                                                                     InterPro; IPR002475;
InterPro; IPR000712;
InterPro; IPR003093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
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                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003093; BH4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; Q07817; 1MAZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=HEART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 RALVADFVGYRLRQKGY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTLAGVVLLGSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIATWMATYLNDHLEPWIQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRTFSDLAAQLHVTPGSAQQRFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RELVVDFLSYKLSQKGYSWSQFTDVEENRTEAPEGTESEAETPSAINGNPSWHLADSPAV 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00452; Bcl-2; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SM00337; BCL; 1.
SM00265; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; PS50062; BCL2_FAMILY; 1

3; PS01080; BH1; 1.

3; PS01258; BH2; 1.

3; PS01259; BH3; 1.

3; PS01260; BH4_1; 1.

3; PS01260; BH4_1; 1.

4; PS50063; BH4_2; 1.

5; PS50063; BH4_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.5%;
                                                                                             ; BCL2_family.
; Bcl_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BCL2_family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 428.5; DB b;
Pred. No. 9.9e-30;
Prematches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                         Scaramuzzi R.J.,
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                                                                                                                                                                                                                                                           Carter
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                                               Matches
                                                           Query Match
Best Local
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                   "Characterization of the bovine bcl-xL gene and related pseudogenes."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF245488; AAK31307.1; -. EMBL; AF245489; AAK31308.1; -. EMBL; AF245489; AAK31308.1; -.
                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ANTI-APOPTOTIC REGULATOR BCL-XL (FRAGMENT).
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                       PROSITE; PS50062; BCL2 FAMILY; PROSITE; PS01080; BH1; 1. PROSITE; PS01258; BH2; 1. PROSITE; PS01259; BH3; 1.
                                                                                                                                                                                       InterPro; IPR002475; BCL2_family.
InterPro; IPR000712; BCl_2.
Pfam; PF00452; Bcl_2; 1.
SMART; SM00337; BCL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9BDD5
                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9BDD5;
                                                                                                                                                                                                                                                                                               Amills M., Bouzat J.;
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                               Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186
            44 QAMRAAGDEFETRERRTESDLAAQLHVTPGSAQQRFTQVSDELFQGGPNWGRLVAFFVFG 103
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 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
 QALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFFSFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGWDTFVELYGNNAAAESRKGQERFNRWFLTGMTVAGVVLLGSL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NGATGHSRSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RELYVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESDMETPSAINGNPSWHLADSPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TE; PS010265; BH4; 1
TE; PS50062; BCL2_FAMILY
TE; PS01080; BH1; 1.
TE; PS01258; BH2; 1.
TE; PS01259; BH3; 1.
TE; PS01250; BH4; 1.
TE; PS01260; BH4; 1.
TE; PS01260; BH4; 1.
                                                          Similarity
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180 A
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BCL2_FAMILY;
                                                                                                        180
20062 MW;
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                                                          39.7%;
53.5%;
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                                               19;
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                                                          Score 401; DB 6;
Pred. No. 1.8e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 425.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                         95DC436F95DABDA6 CRC64;
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nes 59;
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                                                                    Length 180
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RESULT
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ID9 AC Q(
DT 0)
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DT 0
DT 0
OC F
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Best Local
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                                                                                                O9BDX7.
O1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ANTI-APOPTOTIC REGULATOR BCL-XL (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q99N35;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
B-CELL LEUKEMIA/LYMPHOMA X (FRAGMENT).
     Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pec
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yang X.-F., Cantor H.;
"Novel cDNA structure and genomic organization of apoptosis regulatory gene Bcl-x-gamma.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF133281; AAK15455.1; JOINED.
HSSP; P53563; 1AF3.
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Eukaryota; Metazoa; (
Mammalia; Eutheria; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002475; BCL2_family.
InterPro; IPR000711; Bcl_2.
Pfam; PF00452; Bcl_2; 1.
SMART; SM00337; BCL; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                     192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 QAMRAAGDEFETRERRTESDLAAQLHVTPGSAQQRETQVSDELFQGGPNWGRLVAFFVFG 103
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                                                                                                                                                                                                                                                                                                                                                                                                                      E--GNWASVRTVLTGAVALGAL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFFSFG 131
                                                                                                                                                                                                                                                                                                                                                                     ERFNRWFLTGMTVAGVVLLGSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E--GNWASVRTVLTGAVALGAL
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PS01080; BH1; 1.
PS01258; BH2; 1.
PS01259; BH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217
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                                                                                                                                                                                                                                         PRELIMINARY;
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53.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 401; DB 11;
Pred. No. 2.3e-27;
                                                                                                                                                                                                                                         PRT;
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                                Ruminantia; Pecora;
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                                                           Euteleostomi;
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RESULT RESULT Q902988 Q Q00298 AC Q90298 AC Q90298 AC Q90298 AC Q9029 AC Q9
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InterPro; IPR000712; BCL2.
Pfam; PF00452; BCL-2; 1.
SMART; SM00337; BCL; 1.
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                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE=21299061; PubMed=11406282;
Chen M.-C., Gong H.-Y., Cheng C., Wang J.-P., Hong J., Wu J.

"Cloning and characterization of zfBLP1, a Bcl-XL homologue zebrafish, Danio rerio(1).";
EMBL; AF317837; AAK81706.1;
EMBL; AF317837; AAK81706.1;
SEQUENCE 238 AA; 26253 MW; 6E58394933EEFDDB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei; Cypriniformes; Cyprinidae; Danio.
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Last annotation updat
                                                                                                                                                                                                                                     Score 397; DB 13; Pred. No. 5.7e-27;
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01-DEC-2001 (TrEMBIrel. 19, Last sequence up
01-DEC-2001 (TrEMBIrel. 19, Last annotation
B-CELL LYMPHOMA PROTEIN 2.
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"Construction of a robust CHO cell line for biopharmaceutical use.";
submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF404339; AAK92201.1; -.
SEQUENCE 236 AA; 26500 MW; BEDF052EF32CA8B8 CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
MEDLINE-20350651; PubMed=10894153; Rucker E.B. III, Dierisseau P., Wagner K.U., G Wynshaw-Boris A., Flaws J.A., Hennighausen L.; "Bcl-x and Bax regulate mouse reference of the company of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DTRALVADFVGYRLRQKGY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFTQ 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; I Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                               Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 395; DB 11;
Pred. No. 8.5e-27;
                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
            primordial germ cell survival
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                 Garrett L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 236;
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Best Local (
MGD; MGI:88139; Bc121.
InterPro; IPR002475; BCL2_family.
InterPro; IPR007712; BcL_2.
InterPro; IPR003093; BH4.
InterPro; IPR003093; BH4.
Pfam; PF00452; Bc1-2; 1.
Pfam; PF00452; Bc1-2; 1.
SMART; SM00337; BGL; 1.
SMART; SM00337; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50062; BCL2_FAMILY; 1
PROSITE; PS01080; BH1; 1.
PROSITE; PS01259; BH3; 1.
PROSITE; PS01250; BH4_1; 1.
PROSITE; PS01260; BH4_2; 1.
PROSITE; PS0063; BH4_2; 1.
NOW_TER 188 188
SEQUENCE 188 AA; 21126 MW; 4
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InterPro; IPR000712; Bcl_2.
InterPro; IPR003093; BH4.
Pfam; PF00452; Bcl-2; 1.
Pfam; PF02180; BH4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O35843
O35843;
O1-JAN-1998
O1-JAN-1998
O1-DEC-2001
                                                                                                                                                                                                                                                  "A novel Bcl-x isoform connected apoptosis in T cells."; Immunity 7.629-639(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BCL2L.
                                                                                                                                                                                                     EMBL; U51277; AAC53458.1; -. HSSP; P53563; 1AF3.
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=B6/CBA; TISSUE-THYMUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                              MEDLINE=98051053; PubMed=9390687; Yang X.-F., Weber G.F., Cantor H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BCL-X-GAMMA
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MGD; MGI:88139; Bc121.
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Mol. Endocrinol. 14:1038-1052(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 CGAGPGEGPAAD------PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTPGSAQQRFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 RELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEAERETPSAINGNPSWHLADSPAV
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SM00265; BH4; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 05, (TrEMBLrel. 05, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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42.4%; Pred. No. 7.1¢
tive 17; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38;
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RESULT 14
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Best Local
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Best Local
                                                                                                                                                                                                                                                                                                                            InterPro; IPR003093; BH4.

Pfam; PF00452; BC1-2; 1.

Pfam; PF02180; BH4; 1.

SMART; SM00337; BCL; 1.

SMART; SM00265; BH4; 1.

PR0SITE; PS50062; BCL2 FAMILY; 1

PR0SITE; PS01080; BH1; 1.

PR0SITE; PS01080; BH4; 2; 1.

NON_TER 188 188
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01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TYEMBLrel. 16, Created)
01-MAR-2001 (TYEMBLrel. 16, Last sequence update)
01-DEC-2001 (TYEMBLrel. 19, Last annotation update)
BA243J16.1.1 (BCL2-LIKE 1 (ISOFORM 1)) (FRAGMENT).
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                                                                                                                                                                                                                                                                                                           SEQUENCE
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HSSP; Q07817; 1LXL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002475; BCL2_family InterPro; IPR000712; Bcl_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAY-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brown A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE
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                                                                                                                                        11 RALVADFVGYRLRQKGY------
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                                           CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRTFSDLAAQLHVTPGSAQQRFT
                                                                                         RELYVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV
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                                                                                                                                                                                                                                                                                                        188 AA;
                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAC10003.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; BH3; 1.
; BH4_1; 1.
; BH4_2; 1.
A; 26122 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BCL2_FAMILY;
                                                                                                                                                                                                                                                                                                        21029 MW;
                                                                                                                                                                                                            36.6%; Score 369.5; 42.4%; Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.8%;
42.4%;
                                                                                                                                                                                 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 371.5; DB Pred. No. 9.5e-25
                                                                                                                                                                                                                                                                                                      7074B6095145C324 CRC64;
                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      649D914C2D5378F6 CRC64;
                                                                                                                                                                                                            No. 1.1e-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                                                                                               DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11;
                                                                                                                                                                                      38;
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                                                                                                                                                                                                                             Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q90ZH2;
Q1-DEC-2001 (TrEMBLrel. 19, C
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Q1-DEC-2001 (TrEMBLrel. 19, L
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BCL-XL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                     167 WASVRTVLTGAVAL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGDEFETRERRTESDLAAQLHVTPGSAQQRETQVSDELFQGGPNWGRLVAFFVFGAALCA 108
                                                                                                                                                                                                                                                                                                                                              ESANKEMTDLLPRIVQWMVNYLEHTLQPWMQENGGWEAFVGLYGKNAAAQSRESQERFGR 184
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